1 ATGAGCCAGC CCAGGCCCCG CTACGTGGTA GACAGAGCCG CATACTCCCT 51 TACCCTCTTC GACGATGAGT TTGAGAAGAA GGACCGGACA TACCCAGTGG 101 GAGAGAAACT TCGCAATGCC TTCAGATGTT CCTCAGCCAA GATCAAAGCT 151 GTGGTGTTTG GGCTGCTGCC TGTGCTCTCC TGGCTCCCCA AGTACAAGAT 201 TAAAGACTAC ATCATTCCTG ACCTGCTCGG TGGACTCAGC GGGGGATCCA 251 TCCAGGTCCC ACAAGGCATG GCATTTGCTC TGCTGGCCAA CCTTCCTGCA 301 GTCAATGGCC TCTACTCCTC CTTCTTCCCC CTCCTGACCT ACTTCTTCCT 351 GGGGGGTGTT CACCAGATGG TGCCAGGTAC CTTTGCCGTT ATCAGCATCC 401 TGGTGGGTAA CATCTGTCTG CAGCTGGCCC CAGAGTCGAA ATTCCAGGTC 451 TTCAACAATG CCACCAATGA GAGCTATGTG GACACAGCAG CCATGGAGGC 501 TGAGAGGCTG CACGTGTCAG CTACGCTAGC CTGCCTCACC GCCATCATCC 551 AGATGGGTCT GGGCTTCATG CAGTTTGGCT TTGTGGCCAT CTACCTCTCC 601 GAGTCCTTCA TCCGGGGCTT CATGACGGCC GCCGGCCTGC AGATCCTGAT 651 TTCGGTGCTC AAGTACATCT TCGGACTGAC CATCCCCTCC TACACAGGCC 701 CAGGGTCCAT CGTCTTTACC TTCATTGACA TTTGCAAAAA CCTCCCCCAC 751 ACCAACATCG CCTCGCTCAT CTTCGCTCTC ATCAGCGGTG CCTTCCTGGT 801 GCTGGTGAAG GAGCTCAATG CTCGCTACAT GCACAAGATT CGCTTCCCCA 851 TCCCTACAGA GATGATTGTG GTGGTGGTGG CAACAGCTAT CTCCGGGGGC 901 TGTAAGATGC CCAAAAAGTA TCACATGCAG ATCGTGGGAG AAATCCAACG 951 CGGGTTCCCC ACCCCGGTGT CGCCTGTGGT CTCACAGTGG AAGGACATGA 1001 TAGGCACAGC CTTCTCCCTA GCCATCGTGA GCTACGTCAT CAACCTGGCT 1051 ATGGGCCGGA CCCTGGCCAA CAAGCACGGC TACGACGTGG ATTCGAACCA 1101 GGAGATGATC GCTCTCGGCT GCAGCAACTT CTTTGGCTCC TTCTTTAAAA 1151 TTCATGTCAT TTGCTGTGCG CTTTCTGTCA CTCTGGCTGT GGATGGAGCT 1201 GGAGGAAAAT CCCAGGTGGC CAGCCTGTGT GTGTCTCTGG TGGTGATGAT 1251 CACCATGCTG GTCCTGGGGA TCTATCTGTA TCCTCTCCCT AAGTCTGTGC 1301 TAGGAGCCCT GATCGCTGTC AATCTCAAGA ACTCCCTCAA GCAACTCACC 1351 GACCCCTACT ACCTGTGGAG GAAGAGCAAG CTGGACTGTT GCATCTGGGT 1401 AGTGAGCTTC CTCTCCTCT TCTTCCTCAG CCTGCCCTAT GGTGTGGCAG 1451 TGGGTGTCGC CTTCTCCGTC CTGGTCGTGG TCTTCCAGAC TCAGTTTCGA 1501 AATGGCTATG CACTGGCCCA GGTCATGGAC ACTGACATTT ATGTGAATCC 1551 CAAGACCTAT AATAGGGCCC AGGATATCCA GGGGATTAAA ATCATCACGT 1601 ACTGCTCCCC TCTCTACTTT GCCAACTCAG AGATCTTCAG GCAAAAGGTC 1651 ATCGCCAAGA CTGTCTCCCT GCAGGAGCTG CAGCAGGACT TTGAGAATGC 1701 GCCCCCCACC GACCCCAACA ACAACCAGAC CCCGGCTAAC GGCACCAGCG 1751 TGTCCTATAT CACCTTCAGC CCTGACAGCT CCTCACCTGC CCAGAGTGAG 1801 CCACCAGCCT CCGCTGAGGC CCCCGGCGAG CCCAGTGACA TGCTGGCCAG 1851 CGTCCCACCC TTCGTCACCT TCCACACCCT CATCCTGGAC ATGAGTGGAG 1901 TCAGCTTCGT GGACTTGATG GGCATCAAGG CCCTGGCCAA GCTGAGCTCC 1951 ACCTATGGGA AGATCGGCGT GAAGGTCTTC TTGGTGAACA TCCATGCCCA 2001 GGTGTACAAT GACATTAGCC ATGGAGGCGT CTTTGAGGAT GGGAGTCTAG 2051 AATGCAAGCA CGTCTTTCCC AGCATACATG ACGCAGTCCT CTTTGCCCAG 2101 GCAAATGCTA GAGACGTGAC CCCAGGACAC AACTTCCAAG GGGCTCCAGG 2151 GGATGCTGAG CTCTCCTTGT ACGACTCAGA GGAGGACATT CGCAGCTACT 2201 GGGACTTAGA GCAGGAGATG TTCGGGAGCA TGTTTCACGC AGAGACCCTG

FEATURES:

Start Codon: 1 Stop Codon: 2260

2251 ACCGCCCTGT GA

HOMOLOGOUS PROTEINS:

Top BLAST Hits:		
	Score	E
gb AAF81911.1 AF279265_1 (AF279265) putative anion transpor	476	e-133
gb AAF71715.1 AF230376_1 (AF230376) prestin [Meriones ungui	471	e-131
ref NP 000432.1 pendrin [Homo sapiens] >gi 11421915 ref XP	451	e-125
ref[NP 035997.1] Pendred syndrome homolog (human); Pendred'	448	e-124
ref NP 062087.1 Pendred syndrome homolog (human) [Rattus n	447	e-124
ref[NP 067328.1] down-regulated in adenoma [Mus musculus] >		e-120
ref NP 000102.1 down-regulated in adenoma protein [Homo sa		e-115
sp 070531 DTD RAT SULFATE TRANSPORTER (DIASTROPHIC DYSPLASI		1e-99
ref NP 000103.1 sulfate anion transporter 1; Diastrophic d	362	1e-98
ref NP_031911.1 diastrophic dysplasia [Mus musculus] >gi 2	357	4e-97
BLAST to dbEST:		
	Sco	re E
ail8630793 /dataset=dbest /taxon=960	5	23 e-146

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

Expression information from BLAST dbEST hits:

gi|8630793 Human head-neck

```
1 MSQPRPRYVV DRAAYSLTLF DDEFEKKDRT YPVGEKLRNA FRCSSAKIKA
51 VVFGLLPVLS WLPKYKIKDY IIPDLLGGLS GGSIQVPQGM AFALLANLPA
101 VNGLYSSFFP LLTYFFLGGV HQMVPGTFAV ISILVGNICL QLAPESKFQV
151 FNNATNESYV DTAAMEAERL HVSATLACLT AIIQMGLGFM QFGFVAIYLS
201 ESFIRGFMTA AGLQILISVL KYIFGLTIPS YTGPGSIVFT FIDICKNLPH
251 TNIASLIFAL ISGAFLVLVK ELNARYMHKI RFPIPTEMIV VVVATAISGG
301 CKMPKKYHMQ IVGEIQRGFP TPVSPVVSQW KDMIGTAFSL AIVSYVINLA
351 MGRTLANKHG YDVDSNQEMI ALGCSNFFGS FFKIHVICCA LSVTLAVDGA
401 GGKSQVASLC VSLVVMITML VLGIYLYPLP KSVLGALIAV NLKNSLKQLT
451 DPYYLWRKSK LDCCIWVVSF LSSFFLSLPY GVAVGVAFSV LVVVFQTQFR
501 NGYALAQVMD TDIYVNPKTY NRAQDIQGIK IITYCSPLYF ANSEIFRQKV
551 IAKTVSLQEL QQDFENAPPT DPNNNQTPAN GTSVSYITFS PDSSSPAQSE
601 PPASAEAPGE PSDMLASVPP FVTFHTLILD MSGVSFVDLM GIKALAKLSS
651 TYGKIGVKVF LVNIHAQVYN DISHGGVFED GSLECKHVFP SIHDAVLFAQ
701 ANARDVTPGH NFQGAPGDAE LSLYDSEEDI RSYWDLEQEM FGSMFHAETL
751 TAL
```

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION N-glycosylation site

```
Number of matches: 3

1 153-156 NATN

2 156-159 NESY

3 580-583 NGTS
```

[2] PDOC00005 PS00005 PKC_PHOSPHO_SITE Protein kinase C phosphorylation site

```
Number of matches: 2
1 45-47 SAK
2 445-447 SLK
```

[3] PDOC00006 PS00006 CK2_PHOSPHO_SITE Casein kinase II phosphorylation site

```
Number of matches: 11
           18-21 TLFD
      1
      2
           158-161 SYVD
      3
           240-243 TFID
           365-368 SNQE
           459-462 SKLD
           556-559 SLQE
           635-638 SFVD
      7
      8
           691-694 SIHD
      9
           722-725 SLYD
     10
           726-729 SEED
           732-735 SYWD
```

[4] PDOC00007 PS00007 TYR_PHOSPHO_SITE Tyrosine kinase phosphorylation site

```
Number of matches: 2
1 7-15 RYVVDRAAY
2 447-454 KQLTDPYY
```

[5] PDOC00008 PS00008 MYRISTYL N-myristoylation site

		1.0
Number of	matches:	10
1	77-82	GGLSGG
2	78-83	GLSGGS
3	89-94	GMAFAL
4	103-108	GLYSSF
5	335-340	GTAFSL
6	435-440	GALIAV
7	481-486	GVAVGV
8	485-490	GVAFSV
9	581-586	GTSVSY
10	681-686	GSLECK

Membrane	e spann	ing str	ucture	and domains:
Helix	Begin	End	Score	Certainty
1	51	71	0.893	Putative
2	82	102	1.020	Certain
3	107	127	1.729	Certain
4	130	150	1.497	Certain
5	186	206	1.723	Certain
6	228	248	1.517	Certain
7	256	276	1.898	Certain
8	288	308	1.252	Certain
9	338	358	1.568	Certain
10	383	403	1.304	Certain
11	412	432	2.345	Certain
12	469	489	1.997	Certain
13	619	639	1.146	Certain

```
BLAST Alignment to Top Hit:
>gb|AAF81911.1|AF279265_1 (AF279265) putative anion transporter 1 [Homo
sapiensl
         Length = 738
 Score = 476 \text{ bits } (1224), \text{ Expect = } e-133
 Identities = 263/724 (36%), Positives = 428/724 (58%), Gaps = 36/724 (4%)
 Frame = +3
           LFDDEFEEKDR--TYPVGEKLRNAFRCSSAKIKAVVFGLLPVLSWLPKYKIKDYIIPDLL 227
Query: 54
           L + EE R + P + R +CS A+ A++ LPVL WLP+Y ++D+++ DLL
           LNQEHLEELGRWGSAPRTHQWRTWLQCSRARAYALLLQHLPVLVWLPRYPVRDWLLGDLL 74
Sbjct: 15
Query: 228 GGLSGGSIQVPQGMAFALLANLPAVNGLYSSFFPLLTYFFLGGVHQMVPGTFAVISILVG 407
                  +Q+PQG+A+ALLA LP V GLYSSF+P+ YF G + GTFAV+S++VG
           SGLSVAIMQLPQGLAYALLAGLPPVFGLYSSFYPVFIYFLFGTSRHISVGTFAVMSVMVG 134
Sbjct: 75
Query: 408 NICLQLAPESKFQVFNNATNESYVDTAAMEAERLHVSATLACLTAIIQMGLGFMQFGFVA 587
                      A N+S ++ A +A R+ V++TL+ L + Q+GLG + FGFV
            ++ LAP+
Sbjct: 135 SVTESLAPQ-----ALNDSMINETARDAARVQVASTLSVLVGLFQVGLGLIHFGFVV 186
Query: 588 IYLSESFIRGFMTAAGLQILISVLKYIFGLTIPSYTGPGSIVFTFIDICKNLPHTNIASL 767
            YLSE +RG+ TAA +Q+ +S LKY+FGL + S++GP S+++T +++C LP + ++
Sbjct: 187 TYLSEPLVRGYTTAAAVQVFVSQLKYVFGLHLSSHSGPLSLIYTVLEVCWKLPQSKVGTV 246
Query: 768 IFALISGAFLVLVKELNARYMHKIRFPIPTEMIVVVVATAISGGCKMPKKYHMQIVGEIQ 947
            + A ++G LV+VK LN + ++ PIP E++ ++ AT IS G + ++ + +VG I
Sbjct: 247 VTAAVAGVVLVVVKLLNDKLQQQLPMPIPGELLTLIGATGISYGMGLKHRFEVDVVGNIP 306
Query: 948 RGFPTPVSPVVLQWKDMIGTAFSLAIVSYVINLAMGRTLANKHGYDVDSNQEMIALGCSN 1127
            G PV+P + ++G+AF++A+V + I +++G+ A +HGY VDSNQE++ALG SN
Sbjct: 307 AGLVPPVAPNTQLFSKLVGSAFTIAVVGFAIAISLGKIFALRHGYRVDSNQELVALGLSN 366
Query: 1128 FFGSFFKIHVICCALSVTLAVDGAGGKSQVASLCVSLVVMITMLVLGIYLYPLPKSVLGA 1307
             G F+ + C++S +L + GG SQVA SL +++ ++ LG + LPK+VL A
Sbjct: 367 LIGGIFQCFPVSCSMSRSLVQESTGGNSQVAGAISSLFILLIIVKLGELFHDLPKAVLAA 426
Query: 1308 LIAVNLKNSLKQLTDPYYLWRKSKLDCCIWVVSFLSSFFLSLPYGVAVGVAFSVLVVVFQ 1487
            +I VNLK L+QL+D LW+ ++ D IW+V+F ++ L+L G+ V V FS+L+VV +
Sbjct: 427 IIIVNLKGMLRQLSDMRSLWKANRADLLIWLVTFTATILLNLDLGLVVAVIFSLLLVVVR 486
Query: 1488 TQFRNGYALAQVMDTDIYVNPKTYNRAQDIQGIKIITYCSPLYFANSEIF----- 1637
                  L QV DTDIY + Y+ A++++G+K+
                                                 + +YFAN+E +
Sbjct: 487 TQMPHYSVLGQVPDTDIYRDVAEYSEAKEVRGVKVFRSSATVYFANAEFYSDALKQRCGV 546
Query: 1638 -----RQKVIAK--TVSLQELQQDFE-NAPPTDPNNNQTPAN-GTSVSYI----- 1760
                                                     N TS+ +
                    ++K++ K
                            + L++LQ++ +
                                            P
 Sbjct: 547 DVDFLISQKKKLLKKQEQLKLKQLQKEEKLRKQAASPKGASVSINVNTSLEDMRSNNVED 606
 Query: 1761 ----TFSPDSSSPAQSEPPASAEAPGEPSDMLASVPPFVTFHTLILDMSGVSFVDLMGI 1925
                                 ++AP + S + A P FH+LILD+ +SFVD + +
                   S D
                         A +
 Sbjct: 607 CKMMQVSSGDKMEDATANGQEDSKAP-DGSTLKALGLPQPDFHSLILDLGALSFVDTVCL 665
 Query: 1926 KALAKLSSTYGKIGVKVFLVNIHAQVYNDISHGGVFEDGSLECKHVFPSIHDAVLFAQAN 2105
            K+L + + +I V+V++ H+ V + + G F D S+ KH+F S+HDAV FA +
 Sbjct: 666 KSLKNIFHDFREIEVEVYMAACHSPVVSQLEAGHFF-DASITKKHLFASVHDAVTFALQH 724
 Query: 2106 ARDV 2117
             R V
 Sbjct: 725 PRPV 728
```

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
	Sulfate transporter family	254.5	1.5e-72	1
	Ribosomal protein S3, C-terminal domain.	3.3	8	1

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t		score	E-value
PF00916				 1	328	[]	254.5	1.5e-72
PF00189	1/1	651	661	 79	89	.]	3.3	8

```
1 CTGGGTTCCT ATGTGGGGAG GTCATGCTCC CCACTCATTG AGCCCCCCCA
 51 GGCAAACCAC CTGGACAGCC AGACCCATGC AGACTCTGGA GCAGGTGGAG
101 AGGAAGAGTG AGACCACCCC GCCTCACGGG CGGTGAAGGG CCGGCAGCCT
151 CTGAATAGTC TCTGCTAGGA GGTAGAAAGC ACCCTCCCAT CTTAATCATA
201 GTAATCATCG CCACTACCAT TTACTGGGTG CCTATAAAAG GCCAGCCTCT
251 TCATACACAT GATCTCACTG AATCCTCATA GCATCTGCCT GCGACTGTTA
301 TTATCCCCAT TTACAGATGA AGAAACTGAA TCTTTGAACC CAGGTCATCT
351 GGCTCTCAAA CTTGTGCTGT TTTCCCTAAG CCACCCGGTC TCTCATTTCT
401 CCCACTGAAA TGTCTCACAT GCCATTGCCC TTACTCATTT CTGCCCATGT
451 CTCCTCCAAA ACACCATTTA TCAATTCGCT CAACAAGTAT GTGTTGAGTA
501 CACACTAAGG GCCAGGCGAG GGGCTGGGCA CAGGCGCTGG GGGTAGGTTC
551 ATTCTCCCAC CTTCGCTTCT GCTGGGTATC ACCTGTGGGG TCTTGCCGGG
 601 CATCCCACCC TCACCTGTAG TTCAAGTGGA CCTTGGGATC CCAAGACCAA
 651 ATGAATGGAA TGCACCAGCC CAGCCTTCAC CAACTTGAGC ACAATCTTAT
 701 TCATAATAGA AACTCACATT TGCATCACAC TTTACATTTT ACACAACCCC
751 TTCTTATCCA TTAACTCATT TGATCTTCAC AACAACCCTG TGAGATATGT
 801 CTGTTACTCC CACTTTAGTG ATACAGAATC TGAGGTTTGA AAAGTAATGC
 851 TGACCATTCT GCCTCATTAA TAAAAGCAGG ATTAACCCAG GCTCCTGGAC
 901 CCTTCCACAA AAGGCATTAA GCAACCTGCT CCCCTCTGAC AACCTCCCCT
 951 GTCACCCAGG CTCTCCTCTG GGAAGTTGGG GGCATCTCTA GCCCCCAAGT
1001 AGTTACTCAT TTTCAACCCC ATCTCAAATC TTTTGCCAAA CTGGCCACAG
1051 CCACCCCACA CTCCCCACCT CCCAGATACA AATCCTCACT CTAAGCCTTC
1101 CCCATCTCTT TCTTCTCTGT CCTTCTTTCT CTGTGGTCCT CTGAGCAACT
1151 TCTCCCAGCT CTGGGAGGTA GAGGGGAGGT GGGAGACCCA GTAATTGGAA
1201 GAGGGAGGG GAAAGGTTCC TACAGGGAAC TCCTCCGGGC CTCAGGGGCC
1251 CTGGCACTCA GCTCTGCCCA TCTCAGCTCC TGGAACGTCA GCCAGGTTGC
1301 GCAAAAAGTG AGGAGGAGAG GAGCGGCAGT ACACAAGGGT GGGGGAAAGA
1351 TTAGGCACAG GAAGCCGTGG GAGAGAGAC CGGCAGGTGG ACCATCCTGG
1401 TTTCCCCACA CACACCATTG TCCCCCTGGG AAACCTGTTG GTGAAGTTCT
1451 AGATGTCTTA TCCAAGAAGG GTCCTCTTGA GGTCATCTCA GCTATCCCCC
1501 TGCCTCTAGG CAAGCTGTTT TCTGTTTCTT CCAAGCTGAC TGGCTGAATG
1551 GTAGGAGCCT TTCTGCCAGG GAAACTAAGG TCTGGGAAGG GAGTATGGCT
1601 TGTGGGGACA CCAGGGGTCA GGGGAGGGGA GGGTCCACCT GCTGAATCAA
1651 GTGGGGCCTC CTGCCCTCGT GATTCCCCTT TGCCTGGTGC TCAGTGGGGG
1701 TGATGGTGAC GCCACAGGTG TGGAGTGCCA GCCACGTGCT GAGCGCCAAG
1751 CAAAACAGCC AGGGTGAGTC TATGCATCAT CAGTGCCTGG GAAGGAAGGC
1801 CACTGCGAGC AGGGAGTCTG ACGGAAAAAC TTGACAGAGG GAAGGGAGGC
1851 ACCTTGCTTT ATCGGGGCGG GGAAGGCCAG AATAAAACTC TGCTACTGCA
1901 AGGACCAGAG AGAGAAGGCC TGGGCTGGCA CTAGGGAGGG ATGTTCCCTC
1951 ACCCTCCCCT CCTCTGCTTC TCCCAAAGCT TGTAAATGCC CCAGATATGA
2001 GCCAGCCCAG GCCCCGCTAC GTGGTAGACA GAGCCGCATA CTCCCTTACC
2051 CTCTTCGACG ATGAGTTTGA GAAGAAGGAC CGGACATACC CAGTGGGAGA
2101 GAAACTTCGC AATGCCTTCA GGTAACTGGT CCAGAGCCCA GACTTCTGCC
2151 TCCTCTGCTC CCTACCAAAA TCCTTTCTGC ACCAGGACAC GGCTTCTGCA
2201 CTGGTATCCC TAAGATGGGG TTAAGGGAAG CCCTGGGGAA GTGAGGTTCT
2251 GAATGATGAA TTTAAGATCC TACAACCTCA TCTGTACTGA GACCCCCAGG
2301 GAGGATGGGG AGCAGGAGCA AGAACCATCC AGAAGGGTTA TATGGCATTC
2351 CCAAACCCCT GCATGGCATC TCCCATATTC TCAATTCACC CGGGTCTCTC
2401 TGGGTTTGTT AAGGCATGGT AGATGAGCAT CTACGTTATG GAGGGGTGGG
2451 GAGCATCAGA GCCCTTACTC CATGCCCTGT TCCCTCCTTA CAAAAAATAC
2501 CTGAAGTTAC CATCACCCCA GGTTCTTTGT CCTTTCCCTC CCGGATGTTC
2551 CTTCCTCCAC TTGGTCCAGA GAATGCCAAA AGGAGGCCCT AAATTTCTGA
2601 ACTITCCTGA GGGGACCTAC CAGGGTGTAG TCCTACCAGC GCCCAGGGTC
2651 TTTCCACTCT CATCTCCCTG GAAATGCGAT GGTGGGTATG AAACCTTGTC
2701 CCTAAGTAGG CGCTACACAA GGTGATCCAT ACCCACACCC CAGGAGGCTG
2751 GGGCTGCGGG TGTCACCCTC CCCATTCCCA GACTCCTGGC AGACCTCCTC
 2801 TGGCCCAGCT ATAGGCCAAC TCACTCTCC TCACTCCCTT GGGGAAACGG
 2851 CTGATTCAGT TACCTGGATT GAGGTCACTG GCAATGGCTG AAGTGGAGAC
 2901 GCAGGTGGAA CTGGTTCAGG CCGGGGGAAT CACCCACTTG AGTTTGTACT
 2951 AAAAGCCCCA GCCCAGCCCT GTTTCTCTTG GGAGGCTCCA TTTCTGCCCA
 3001 GTTACAGTCT GTCCTCACAG CTGTGCTCCT CAGACAGGTG GTCTCTGCCA
 3051 GTCTTTGTGC CCAAGACTTT AGGGCACAAA GTCTGAGGAT GAGAAGATCT
 3101 GCTATTGTCC TAAAAGATTA GGATAATGAA AGCTGTAAAG GGATATAGCA
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3151	AACTAACAAT	TCCTATGATA	CTGGCATGAG	AGCCTTGAAC	AGTGCCTGGC
3201		TGCACCAATA		TCATGAATGA	
3251	GAATGTCTAG	AAAGCTAATC	CCTCTCAGCC	TCTGTTTCCA	GTTCTTCTTT
3301	CAAGCTTCAG	ATTGCTTTGC	CCAACATACA	GCAGACTTGC	AAGTAAGGTT
3351	GGGCATGGAC	TAGCCCTCAA	ATGAGTTGTT	TTTCTTTCCC	TAGCCAGCTC
3401	TCTATTCATA	AGTCCGGCTT	TCTCTGCCAC	AAACAGACCT	GATGGAGCCC
3451	CTGCAGGGCT		TCAAGCAAGG	CTTTAGAGTT	GCATTAAGCA
3501	ATTTATCCCC	CGTCCACCTC	CCCTTCCAGC	ATCCCAGGGA	TGGCAGAGGC
3551		CCCAGAAGGG	ACAGGGGGTA	AGATATTGAT	GATGATGCTT
3601	TTTCTTGGAG		AAGAGAAAAT	CTGCCCAGAC	TTTCCAAGGT
3651	ACAAAGCATT	GTCTTTGTTG	GTTTCAGTCT	TGGGTGACAT	CCAGGGGACC
3701	GAGTGTCAGG	GAAACTATTG	TTGAGCAAGA	GCAAAGAGCA	GGAATTGGTG
3751	CTGGGCAGGA	AAGGAAGCCT	CATCAGAGCA	GGCCAGTGAG	TCACCAAATG
3801	GGCCCTAAGT	ATTTGAGTTC	CCTCAACTGG	GAGAAGGAAA	GCAAATGCCC
3851	CTCACCCACT	TCCAGTCATC	AATCCACCGG	CTGTCACCCT	TGAGTTTGTA
3901	AGCCCTTGTT	CCTACCGCTC	CTGAGTTTCT	ATGAAAGGAC	CTTGAGGTGT
3951	TCAACAAACA	GGGAAGGGAT	CAACTCTCCC	CACCCTGCGT	TGACCAATGA
4001	ATTCTTCCCT	CCTCTGCTGC	CCAGTGAATT	AACAGGAGAA	AGAACTCCGG
4051	TATTGGAGTT	ACCACACATA		AGTCAGCAGA	
4101	CAGGAACAAT	AGAGCCTTCC	TTTTCAAGGA	AGTTCTAAGA	AAAATGGCAG
4151	CAGGCAGGCC	CCACTCGGGT	GTATTCACTC	ATTCATTTAT	TCAACAAATA
4201	TTTACTAAGT	GCCCCTGTGC	AAGGCTCGAG	GTGTACAAAG	ATGAACAGGA
4251	GAGCTAGACT	TCTTGCCATG	CGTGGTGGGG	TTTGCTGCCT	AGTGGGAGAG
4301	ACAGACAAAA	AGCAAGGAAT	GCACACACAG	GATGCACACA	CAGCGGCAGG
4351	AACCAAGGTG	CAGTTACCCA	GGCCTGGGAT	CAGACAGACA	
4401	GAGACTTTCC	CAGAGAAAAG	CCATCTGAGC	CAAGGGATGG	
4451	TCCGAAGGCT	GAGCCACCAT	AACACTCATA	CCTTTAAGCC	AAGTCTTATA
4501	AACTCCCCAG	GTAAGCAGCT	GGCAGTCAGA	AGACCTCCAG	CTAATGCCCA
4551	GGACAAGTTG	ATGAGCTCTC	AAGAAAAAGT	TCCTGCCTTT	TCTTCTCAAT
4601	ATCCCTGGCA	CACAGTTCAG	TGAATTTTGA	ATGAACCAAT	GAATGAAATG
4651	AGCAGGATAT	GATAATCCCT	CTCCAACACG	GAATGTCCAA	GCCATGCAGA
4701	GCCGACTGGA	AATTTTCCCC	GTTCCCTTCC	AGATGTTCCT	CAGCCAAGAT
4751	CAAAGCTGTG	GTGTTTGGGC	TGCTGCCTGT	GCTCTCCTGG	CTCCCCAAGT
4801	ACAAGATTAA	AGACTACATC	ATTCCTGACC	TGCTCGGTGG	ACTCAGCGGG
4851	GGATCCATCC	AGGTCCCACA	AGGTGAAGGG		CCAGGCCTGG
4901	ATTGCCACTC	CCCTCACCAT	TCCTCTCCTC	ATCCCCACTC	
4951	TGATCCCCAT	AAGCTAGTCA	TGCTGCTGAG		
5001	GCAGGCATGG	CATTTGCTCT	GCTGGCCAAC	CTTCCTGCAG	
5051	CTACTCCTCC	TTCTTCCCCC	TCCTGACCTA		
5101	ACCAGATGGT	GCCAGGTAAG	GCCTCTCCCC	TCTGGGCAGG	
5151	CAGACCACAA	GGATGGGAGG	TGTGGCAAAG		AGATTTTCCA
5201				GTCCTAGGGG	
5251	GTGAATGTCA	TTTCCAGGTC	CTCGGTGACC		CACTGAGCCT
5301	CTTTGAGTTC	AGTTAGCATT	ACCTGTTCCA	TCTTCCTCCT	AGGAATGAGA
5351	GGAAGACTTA	GCAGAACAAG	ATATACCATA	TGCTATAACA	TGCTTAAACA
5401	GATGTGAGAA	ATCACCATCT	AACTCCCTGG	TTGGTCCCAG	CCGGCCACTA
5451	CAGGGACATT	TGGACTTCTC	TGGTGCTAAG	TGAGATGGAG	GAAAGCCTGG
5501	TCACAAGGGC	TGGTTTCTGG	TTCAGGCTCT	GCTTATATTT	CITATITUIG
5551	AGTTCATTTT	CTCACGTGTC	CTGTATGACA	ATATTGACCA	TIGGGGIAAA
5601	AGCACCTTGA	AAAGCATAGA	TCATGGTTAG	AGTGAGTGGT	TGTTATTATT
5651	GTGTTGGAGA	AGAGCCTTGG	AGGTGCAGGG	ATCCATCCC	. CIGGGGICGC
5701	GAAGCATTCC	TGGGCCCCTT	TCTGGTTTCC	ATCGGTGTGG	CCCEENTCAC
5751	TGATTTTTGC	TGGCTGGGTG	GGGCACCACA	GGTACCTTTG	CCGITATCAC
5801	CATCCTGGTG	GGTAACATCT	GTCTGCAGCT	DECUCCAGAG	· ACCACCCATC
5851	AGGTCTTCAA	CAATGCCACC	AATGAGAGCT	ATGTGGACAC	, AGCAGCCAT , mcacmcccam
5901	. GAGGCTGAGA	GGCTGCACGT	GTCAGCTACG	CTAGCCTGCC	, ICACIGOCAI
5951	CATCCAGGTG	AGGGGGCAGC	CCCCAACCCT	GUTAGAAGGG	TO THE TOTAL CONTROL OF THE TOTAL CONTROL OT THE TOTAL CONTROL OF THE TO
6001	CCCTGCCCCT	CCCTCAAAGC	CTTAGCTTTG	ALGUTAAATU	CCCACCCTCA
6051	GGCTGGGTGT	GGAGGCTCAT	GCCTGTAATC	CAGCACTTI	. GGGAGGC1GF
6101	GGAGGGTGGA	TCACTTGAGG	TCAGGAGTT1	DAGACCACCI	
6151	GATGAAACCC	CATCTCTACC	AAAAATACAA	AAATAATUUA	Z CDCDDTCDC1AC
6201	TATGCGCCTG	TAGTCCCACC	TACTCAGGAG	THE TENEDOS	CUSCACOVO
6251	TGAATCCGGG	AGGCAGAGG'I	TGCAGTGAGC	, IGAGATUGU	, CCACIGCACI

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6351 AAAAAAAAA CCCAAGTTAG GGCTCACCTC CTCCCTCCTC CCCATCCCAG
6401 GGCTAAAGTG AACCTTGAAA ATTAACAGTA TCTCCTCATC TGCATGTAGC
6451 AGGACCATAC AAAAAAACAA CAGCTGTACC TGGTTAAACT GTCCTGAGCT
6501 TTAAACCTGT AAAAGACTCA CAGCCTCTCT CCATTATCCC GTGGAGAAAC
6551 CCAACTCTCT GCCAGCATAG TCTTGCAGAC TGCTAATTTT CTCTAACATC
6601 CCTCACTCCG CTCCAGCCTC CTCTGCTCCA AGCCACAGCA GCAGTTGCAC
6651 AACATAAATT GAGCTTCTGC AAATGGTTGC AAAGGATTCT GCTAGGTTTT
6701 ATGAAGGGAA GCACAACATG ACAGAATGCA AGAGCAAAAC ACAGTCCCAG
6751 AGAGCGCCTT TTCATTCACT CATTCATTCG GTTTTGTGCC AAGAACTAGG
6801 CTAAACCCTG GGATACAAAG ATAAGTAAGA AAGAGGTCCA ATTCACAAGT
6851 TGCTCACAGC CCAGCAGAGG AAGGAGCCAT GTCAACAGAT AAATTTGTAT
6901 GCAGTGAGAT AAGCAGCAAA GTAGAGCCAT GTACAAAGAC TGTAGGGACA
6951 CAGAGCAGAG TCACGGAGGA CCTCAAAGAG GAGGTGACAC TCCACCTCTC
7001 TTAAAGGATG AGAACTTAAC CAGGAACAAG GTATACAGAG GATGGTCCAG
7051 GCAGAAGGGA ACAGTGCCTA AAAACACTGA GGCCTGAGAG AGTGTGATCT
7101 GCGCAGGCAA AGTAAGGGGC TTGGTGTGGC TGGAGGGTAG AGGGCCCAGA
7151 AGAGGATGGA AAAGTAGGCA GGAGCCAGAC AATGAGATCT GGGGTCTGTT
7201 CTCTGACAGC GACTTTGGGT CTGATTGGCA GTTTATAAGG ATCGTTTGGG
7251 CTACACAATG ATGAGTGGGA GGTGGATTAG AATCAAGGCA GGGGACCTGT
7301 TGGGAGACTC TGCAGAGGCC CAGGCAGGAA TAATGCAGGC GAAGACCAGG
7351 TAGAGAAAGA GATGGGGCTG GACTTGAAAA GAATGTTTTA CCAGGAGCTT
7401 GGTGATAGAC TGGATGTGGG AGGTAAGGGA GGATGACTCT CAAGTTTTTG
7451 GTTGGGCAAC CAGGTTAATG ATGGTGTCAT TTACTGAGAG AGAAAACACT
7501 GGGGGAGGAC TAGACTTATT TTACAGATAA GCCAAAGCCA GAGAGGTGAT
7551 GTGACAGAAA GGCCCATGCT CTAAAGGAGC TGAAGGTCTG ATGGCAGCCA
7601 TGTAGAGCAC AGTGAAGGC AGGTGAAGGT CACAGATGGT CCAATTCCCT
7651 CAAGCTACTG CTACGCTAGG ACTGCACGGA GCTCCAGACC TGCGTGTGTG
7701 TGGGGCGGGT CGTTGGAACT GCTGAACCAC ATTGGTCTTC CGCCACCAAC
7751 CACCCTTTTC CTCCTCTCAG ATGGGTCTGG GCTTCATGCA GTTTGGCTTT
7801 GTGGCCATCT ACCTCTCCGA GTCCTTCATC CGGGGCTTCA TGACGGCCGC
7851 CGGCCTGCAG ATCCTGATTT CGGTGCTCAA GTACATCTTC GGACTGACCA
7901 TCCCCTCCTA CACAGGCCCA GGGTCCATCG TCTTTGTGAG TCTGGGGATG
7951 CACCCCTGCC ATTGGAGCAA GGCTCCAGCA GACACATGAG GAGGATGTAC
8001 TGTTTTAAGA TGTCGTGAGC TCCTCATTGC AAGGGCTGGC TTAGCTGTTG
8051 TTCAGAGAGG ATTCTGAGGG GGTTTCTGTC TTGGGAGGGT CAAAGTCATG
8101 ACTCACAGAG GTTCTTGGTA GTTAATACCT GCAGAAAAGA GCTGTACATT
8151 CTCCGCCAGT TCCCCATTCT AGTGCCTCAA CCCCTCCCTG CCTGGAAAGT
8201 CCTGCCTTAT GTCTAATCTC CATCCCTCCT CCTTCAGCCC AAACTCTTCT
8251 AAAGAAAAAG AAAGCATTCC TTTTCTAGCA CAAGTTCCCC ATGTGCCTTT
8301 TGGGAAAGGG CGGTGGGCGA CGGGACAGGG TTCCTGATCA GGGTTTTAAT
8351 TCTGTCTTGG TGTGCCTCCA TTAGCTTTGA TGGCATCCCT TCCCTGGGTC
8401 AGACACCCAA AGGTGGGGTA TTATGGGAAG AAGGGGTGGG AGCCTGTGAG
8451 CATGATGCTC TTTCCCCCAG ACCTTCATTG ACATTTGCAA AAACCTCCCC
8501 CACACCAACA TCGCCTCGCT CATCTTCGCT CTCATCAGCG GTGCCTTCCT
8551 GGTGCTGGTG AAGGAGCTCA ATGCTCGCTA CATGCACAAG ATTCGCTTCC
8601 CCATCCCTAC AGAGATGATT GTGGTAAGGA CCTTGTTCAG AGCTGGGATG
8651 TTGGGGGGCC AGGCTGTGAG ACGAGGAAGC CCCTACCTTT CCTCACCCCA
8701 TCCCCTCAAC TGGCAGCCAG TGGGACAGGA AGTCAGTTGT GAATCCATCC
8751 CATCCCCCGT ATGTGGCGTT TCCTCTCTTT CTACTGCTCT AATAATTCCC
8801 CCTAAGGAGG CAGGGGAGTG GGATTCAGGG TCCCCAGAGA AAAGGGAGAC
8851 TTGAGAGAGA CGCCTGCCCT GGCCCCACCT TAGGGCCAAT CCCCATTCTC
8901 CACTCTGGGG TTTGCAGGTG GTGGTGGCAA CAGCTATCTC CGGGGGCTGT
8951 AAGATGCCCA AAAAGTATCA CATGCAGATC GTGGGAGAAA TCCAACGCGG
 9001 GTGAGTCCAG GTGGCCCAGA AGCCTGGCCC ACCCGCACCT CATGCCCCAC
 9051 TAAGGCCTGA GCTCGGAGAG GGAGACAAGA TGAACTCTAT GAAAGTGCAG
 9101 TCGAAACTGT ATGACACTGA CCATGTATGA ATTATTACTA TTACCGTTTC
 9151 CTGAGAAGGG CCGCACAACC AGCCAATGTA GGCTATTTTA TGAGAAATGA
 9201 GTCTTAACTG CCACACTCCC CTTATAAATC TCATTCAACT GATGCTGTTA
 9251 AACAAAGCCT CTCTGAACAG CCGCTTGCTG GCTCTTTGCC TTGCTCTAAT
 9301 GCATTGGTTC TTTGTCCATG TAGAAAGGGA ACTATTAGGT TCAACCAGAT
 9351 TCATGAAGCA TCCACTCTGT GCCAGGCACC ATGCTGGGCC CTGGGAGGAG
 9401 AGGGGTGACG CTTGTCCTGC AGGGTTGGAA CAGGCAAGGG AGGGAAGACC
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FIGURE 3, page 3 of 20

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9451 ACATAGCACC AAAGGTCTAG GGGTCTGTGG ACTCGTGAGC ATACAGGGTT
9501 CAGAATCTGG GAGTTAACAA ACGAGGCCCT ACCACATACT GGCCCGGGGA
9551 CCTTGGGCAA GTTAGGTTCT CTCAGCCTCA GTTTCCTCCT TTGTAAAACA
9601 GGAGTGATGG TCCCTACCCT ATGGGGTGGT GCTGAGGATT CAGACTGGAT
9651 GGGATAACTT AGGCAAAGAT CCCGGCACAC CATGGGGGCC TGGCTGGTCC
9701 CTGTGGGCTG GTGAAGGACT TGGCTGCCCT CCCCACTCAC ACCCTTGGGT
9751 TCTGCCTCCT TCCTGGCTCC TCGGCAGGTT CCCCACCCCG GTGTCGCCTG
9801 TGGTCTCACA GTGGAAGGAC ATGATAGGCA CAGCCTTCTC CCTAGCCATC
9851 GTGAGCTACG TCATCAACCT GGCTATGGGC CGGACCCTGG CCAACAAGCA
9901 CGGCTACGAC GTGGATTCGA ACCAGGTAGC TCTGGCCACC CCCGGCAGGA
9951 CTGGGCAGGA CAGGTCAACT CAGGCCTGGC ATGACATATC TTGGGTGGGG
10001 AGATCATTGG GCTGAGGTGA GGCAGGCTGC CTCGAGTGTG GGGGATAGGG
10051 GGTCCTCTGA CCCTAAGAGG CTGACCTCCT CTTGACTGGG AATGTGTGAC
10101 TTTATAGCCA CTGGGTCACT CTCAGGTCTT AGGCCCACAG TCCAGCTTGC
10151 ATGCCTGACT GCACTTGGTC CCCGTGCCCC CCAGCCCCAC ACTGGCTTCT
10201 AATCCTGTCC CCTCCCTGCA GGAGATGATC GCTCTCGGCT GCAGCAACTT
10251 CTTTGGCTCC TTCTTTAAAA TTCATGTCAT TTGCTGTGCG CTTTCTGTCA
10301 CTCTGGCTGT GGATGGAGCT GGAGGAAAAT CCCAGGTGAG CCTTGTTCTA
10351 GGGGAGTTGG GGGGAGGTGG TAAGAGAACA GTTGCCCCAA AAAAGCCTGG
10401 GCACTGCAAG CCAGGCCAGC TCTTCTCCGA CCCCTTCTTC CCGTACTTAG
10451 TCTCCACTCC ACCAAAGCCA TGGATTGGAA ATAAATCAAG AGCAAAAATT
10501 TCACACCTTC CCTCTATCCC CAACTCTTTC TCGGAATAGG TGGCCAGCCT
10551 GTGTGTCT CTGGTGGTGA TGATCACCAT GCTGGTCCTG GGGATCTATC
10601 TGTATCCTCT CCCTAAGGTA AGAGCCCAGC CATCGAGCAG AAGTCAACGA
10651 AAGACTCCAA TAAGAACAAT CCCTGAGAGT TGTGTGGCAC TTTACGGACC
10701 ACAAAGTGCC ACTGTTGTCA TACTTAGTCT CAACCACAAA CTGTGAGGTA
10751 GACAATGCAG GTTTTATCCT CCCCATTTTA CAGGTGAAGG AAACTGAGTC
10801 TGAGAGTCTA AGTAACCTTG TCCATAGTGA GGCAGCTTAC AGCGCAGGGC
10851 TGGTCCCAAA CTCCAGCCTT CTGGCCTCAG AGTCTAATCC CTAGGCAACA
10901 TTTGCACCTA CCCACGAGTA CCAGGCTCTT ATATAGCCCA GCTAGGAGGG
10951 CTCTAGGCAT GCGTCATTTA GAGATGAGGG AAGAGAGATA GGGAAAGGAT
11001 GGGGCCAGGA AGGACCCCAT GGCTCTAACG CCAGCACTTT CCAAACCTAA
11051 GGTCGAATGC AGAGATTTGG GGGATCAGCC AGGGGAGGTG TTCCAGAACT
11101 CCGTCTCTGT CCTGCCAGGC CTTGGGGTCG GGTATGCGCA GGAGGGCAAA
11151 AAGAAGGGGA GACCCTGGGG TCCTGGAGCA ATGTTCTGCT TCTCTAGTCT
11201 GTGCTAGGAG CCCTGATCGC TGTCAATCTC AAGAACTCCC TCAAGCAACT
11251 CACCGACCCC TACTACCTGT GGAGGAAGAG CAAGCTGGAC TGTGTAAGTA
11301 TCGGGCAGCC TCTGGGTACT GGCCATGCCC CTGCCCTCTC CTCCAACCCC
11351 ACAGCCCTGT CAGCCCTGTC CTAACAATGA ACCCTCTAGT CTGCTGCTTC
11401 CTAATTAGCA TGAGATGAGT GGTTAAAAGT CCGAGTTTCG AAGTGAAACA
11451 TCCTATGTTC AAACCCTAAC TCAGCCATCT GCTGGCTCCA TGGCCAATAG
11501 CAAGCCCCTT AACCTTTCCC AGTCTTGGTG TCTTAACTGG GCAAATGGTT
11551 ATTTTATGCT CTCTGCCTCC CAGGGTTTTC TATGAAGAAG AAGCAAGGTA
11601 ATACAAGTAA ACATGTTGTC TACATCGTAT TTTATACTCA ATAAAGCTTA
11651 GCTATGACTA CTTTATGACA TACAGCTTTA AAAAACAAAA GGAAATAGTT
11701 TGTATTTTAA AAAAAAACCT AGAACATAAA GCCAGAGGAC CAAAATCTTG
11751 AGCAAGTTAC TAGACTTCCC TGGGGTTCTA TTTCCTCATC TGTAAATGGG
11801 GGTGAGACTC ATGCAGTCAT GGTTGCGTCA AACGCTGGTT CCGAGGATTA
11851 AATGAGATCC CAGTGGGAAA ACACCGCATG AGCGCAAACA TTCTGCAAAC
11901 ATGACTTATT GTCCTGATTA GTCACACACT CCACCGCATC ATCCGCTGGG
11951 CATAGTAATG AAGGCCAGTG TGTTTTGACG ACACTGCCTT CTCTCCATTT
12001 AAGCCCCACC ATAACCTATG GGAGAGGATT TACTAAACTT TCTTAACGGT
12051 GATGAAACCA AGGCTCAGAA TGGTTAAGTA AATTGTCAAA GGCCACAGAG
12101 GTAGGGAGTG GTAGAGTCTG GATTAAAACT CCAAGTCCTG GACTCCAGAC
12151 CTCTAGGCTG TACTGTCTCA TAGGGAAGGC AGTCTCACCC ACCTAGGGCA
12201 GAGAAGAAA TCCTTAAAGC CAGAGAAGTG AGTGGCTCAT CTGTGGTCAC
12251 CCAGAGAGAC AGTGATGAGG ACAGGGAGAA AAATTATACC TCAGTTCCCA
12301 GCCCAAGGAT CTGCTTTGAC CATAACCCAA CAAGCCCCCG CTATGGTGGT
12351 ATTTCCTTAG GTTCATATGG CGGCTTTTGT TTCCATTTGA TCTTCACAGC
 12401 AATTCTCTAC AGGAATCTGG GCAGATTTAT TTCCTTTAGA GGAATTTCCA
 12451 GGTCTTAAAA TCTATAGGGG GCAACTATCA AAACTTCACC CAATGTTGCC
 12501 CCCTACCCAC ACACAAAACC AGGCCCCCAG CCGATCAGAA AGCACTGCTG
 12551 AGCTCCTGTC AGGGCCCACG CAGCTCGCTG TGAGACAGAG AGAGGGAACT
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12601	CACATTTATT	GATCACCTAC	TGAGCATCCA	TCACTAGGCT	AGGACCGTCA
12651	CATTCCTTAA	CTTTTGAATC	CTTTCATGAG	GTAGGCATTA	TTATTCTCCT
12701	TTTGTTTCAC	ATAGCCATTA	AAGAACAAAA	TTTGGGGCTG	GGTGTGCTGA
12751	CTCACACCTG	TGATCTAGCA	CTTTAGGGGG	CTGAGGCAGG	AGGATCGCTT
12801	GAAGTCAGGA	TTTCAAGGTC	AGCTTGGGCA	GCTTAGCGAG	AGCCGTCTCT
12001	AGAAAAATAT	AAAAGTTAGC	TGGGTGTGGT	GGCACGTGCC	TATAGTCCTA
12901	ACTATTCAGG	AACCTTACCC	GGGAGCACAA	CTTGGGTTCC	AGGGTTTGAG
12051	GCTCCAGTGA	CCTCATCTTC	CCACTGCACT	ACAGCCTGAG	CAACAGAGCA
12951	AGACCCTGTG	CUCCLANA	CARTICATACA	AACACATTTT	GAACCCAAAC
13001	AGATCTGACC	ACTOCAAAAA	CCTCTTTTTC	AMCACATTIT	CCTGTGTGCT
13051	GGGGCTTCTA	CAAGATGCAT	ACACAACATC		
13101	AGGGAAAGAG	CTAAAAACAC	AGACAAGAIC	AGGCAACCAC	AUTOPPACCA A A
13151	AGGGAAAGAG	GAAAGTGTAA	CCAAAGCACA	AAIACAIAAA	CTTCTACTAA
	AATGCTATTT	AAAGAAAAA	AAGAGAAGAG	AGGCICIGAG	CACCUTCUTT
13251	CAGAGAATGG	CCTTGGCTAA	TCCAGGAAGA	CIICCIGAAA	CARCECCCEA
13301	TTTCCCCAGG	TCTGCTTTTG	ACATCTCTCT	TTTCACAGIG	CHICIGGGIA
13351	GTGAGCTTCC	TCTCCTCCTT	CTTCCTCAGC	CTGCCCTATG	GIGIGGCAGI
13401	GGGTGTCGCC	TTCTCCGTCC	TGGTCGTGGT	CTTCCAGACT	CAGTIGIAAG
13451	TGATAGCTTC	CGCCCTCCTA	GGCCCACAGT	CGGTTCCCTG	GGUCAGUCCG
13501	CAAAGGGCTT	CCATGCCACG	GCCTGGCTTA	GTCCACTGTA	CCTTCCACCI
13551	CTGGGCCTGG	CACTGGAGGT	GCTGCCAGGC	CCAAAGAGAG	CCCAACCCAG
13601	CCAGGACTGT	GGGCACAGTC	TGGGCTGTTT	GACTTCCCAT	ATCTTGAAAA
13651	CCCCAGAGAA	AGCCAGCATA	CTCTTGCTGG	GGATGGCTGG	GGAGAGGGCA
13701	GTGGCAGAGA	AAGGAGGGCA	AGGGCAGGTG	GTGAGATTCA	ACATCCTTCC
13751	AAAGACATTG	CCAGAACCCC	AAACCAAATG	GGACCCCACC	CCAGGAGAGC
13801	GCCAGGGTGG	AAGACAGAAG	CTGTGTTCTA	CACACTGGGA	GTATTACAGA
13851	GAAGGGGTCT	TGGCCAAGGC	AGGGAGTACG	CTGAATGTTG	GGGGAATCCT
13901	ATCTTCTCTT	CTTGAGAACT	CAGAACAAGG	AAATGATGAC	TTCAGGGCGA
13951	CTCCCACCAC	TTCTCCCACC	ACTTCTCTCC	CCTGCCCTGT	GGTCTGGGAG
14001	CTATGTCAAG	GACCTGCCTG	TCATCCTCAT	AGTTATAGGA	GGCCACAGGC
14051	CACCAGACAT	GTGTCTCCAG	TGCAAAAAGA	CAGACACAGC	AAGTCTGGGG
14101	GTGAGGACAG	GACCCCATCC	TACCTTGGCT	CTGCCCCCGC	CCCAGCAGGG
14151	GCACCCTTCC	AGGCCCATGT	GCCATTAGCA	TTCTCTTATG	TTTTTCTCTT
14201	CCTGCTTCAT	CCAGTCGAAA	TGGCTATGCA	CTGGCCCAGG	TCATGGACAC
14251	TGACATTTAT	GTGAATCCCA	AGACCTATAA	TAGGGTAGGT	AATTCAAGCT
14301	TATGACCTCC	TTCTTTTGCT	CTGCACCACC	CCAAGAAGAG	GTTGCTTTTT
14351	AAAGCCAATA	AAGACATTTC	TGCAACTTGA	GCTCAGTCTC	CCTGTCACAG
14401	GCCCAGGATA	TCCAGGGGAT	TAAAATCATC	ACGTACTGCT	CCCCTCTCTA
14451	CTTTGCCAAC	TCAGAGATCT	TCAGGCAAAA	GGTCATCGCC	AAGGTAAGGC
14501		GCGACCAGAG	GCTCTGGACA	GAGAGTGGCC	GGAAAATGGA
14551	AGCAGAAGGG	CGGTGGGAGC	TGAGAATAGG	CCACTCCCAT	AGAGGGTGGA
14601		GCTGTTGGCT	CTCTCCCTGC	AGACAGGCAT	GGACCCCCAG
14651		TAGCCAAGCA	AAAATACCTC	AAGAAGCAGG	AGAAGCGGAG
1/701	AATGAGGCCC	ACACAACAGA	GGAGGTCTCT	ATTCATGAAA	ACCAAGGTGA
14751	ATGAAGGCCA	GAAGCAGCCC	CGTGCCCTGC	TCTCCTGCCC	ATTCTGATAC
14901	TGCCCCCTGT	TACTCATGGT	ACCCTGGGGG	CCCCGCTTCC	CACCCTGACA
14951	GGCAAAGACA	GAAAGTCTCT	GGGAACACTG	CCTGGTGGCC	GCTGGGCATT
14001	TTTCTTCTTT	TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	TCTTTTTAGA	GATGGAATTT	TGCTCTTGTC
14051	ACCCAGGCTT	CACTCCAATC	GCGTTATCTT	GGCTCACTGC	AACCTCCACC
14901	TCTGGGGTTC	A A C C C A T T C T	, CCTGCCTTAG	CCTCCCAAGT	CGCTGAGATT
15001	. ACAGGTGCCA	CCACACCCAG	: CTAATTTTTC	TATTTTTAGT	AGATATTGGG
15051	TTTCACCATG	TTTCCCCACCCAC	TCCTCTCAAA	CTCCTGACCT	CAGGTGATCO
12101	ACCTACCTTA	CCCMMCCAA7	CTCCTCCCAT	TACAAGCCTG	AGCCACTGCC
15151	. CCCAGCCTGG	CCV managanaca	T TOTTCCATCE	GGTGCTACCA	TCTCCCAGG
15201	. CCCAGCCTGG	ACCCCCAACC	CCCTTCTCTC	₹ ₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩₩	AAGATAGGA
15251	AAGCCACTGA	ACCCCCAAGO	CDACCCACACA	CCCCAACAG	DCTCDATTT
15301	ATGGCCCATG	GACTTTTGAL	A CAMOUCAGAG	ACCCTCCCC	GGCCATGGC
15351	CTGGGGAACC	CAGGCAGCCC	ACCUMUNACAN	T WAGGERGAGE	: GAGAATCAC
15401	GTAATCCTTC	TAATCCCAG	ACTITAGGAC	B CCCCVVCCM	CCCABACCC
15451	CTCATGAGTT	CAGGAGTTC	AGACCAGCC	L GUUUHAUGIU	CTCCCCACC
15501	GTCTCTACTA	AAAATACACA	A AAAATTAGU	AGGCGIGGI(3 GIGGGCACC.
15551	L GTAATCCCAG	GTACTCAGGA	A GGCTGAGGCA	A COGNOTION A	, 400760000 , 1197400000
15601	L GAGGCAGAG	TTGCAGTGA	G CCGAGATAG	L GCCACTGCAC	A CTCTCTCCCC
15651	L GCAACAGAG	GAGACTCTG	r Crcaagaaa	L CACCOMMON	- 461616666 - 461616666
15701	L GAGGGGCTT	CTCCCAGAG	A GAGTGGGCT".	r GAGGCTTCAC	3 1GCC1C1C1

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15751 GGCTGGGTCC TCTGACTTTG TCTGGGTTGT AGGAGACCAA GTTTGCAGGC
15801 CCTGCCTAAG AAAGGGCTTT GGGAGAGGCC TCTCTGGTGG AGCTTTCAGG
15851 GTCTGTGTTC ACCATCACCG AGGCGAGTTA TTCCCCTACA CCTACACCCT
15901 CCATGCCCCT GCTTCAGTCA CAGCAAGGTC TGGCTCAGTC TGGTGGTCCC
15951 TGACTCTGCC CACTGTCCCC ACCCTTCCAG ACTGTCTCCC TGCAGGAGCT
16001 GCAGCAGGAC TTTGAGAATG CGCCCCCAC CGACCCCAAC AACAACCAGA
16051 CCCCGGCTAA CGGCACCAGC GTGTCCTATA TCACCTTCAG CCCTGACAGC
16101 TCCTCACCTG CCCAGAGTGA GCCACCAGCC TCCGCTGAGG CCCCCGGCGA
16151 GCCCAGTGAC ATGCTGGCCA GCGTCCCACC CTTCGTCACC TTCCACACCC
16201 TCATCCTGGA CATGAGTGGA GTCAGCTTCG TGGACTTGAT GGGCATCAAG
16251 GCCCTGGCCA AGGTGAGGCC CTCGGGGACA GCAAGCACCA CCCACTCCAC
16301 CCCCTCCGCT CTGCTCTCCA CATTCCCTTT CCTGGGAGCC CTCATTTCAG
16351 GAAGCTGAGG GAGGAAGCTC ACTGGGGAGA CTAACAGCTC CTAGGAATCC
16401 CTCCTTTCCC CAGACGCCAC CAGGTTGAGA CATTCTCCAC AGAGCAGGCC
16451 CAGACGGCCC ATGACAATGA GTGGCGGGAC AAGTCTACCA GAGTTTCAGG
16501 CCCCTGTGCT CCCAACACCC CCAGCAGTGG CCATCCCAAG TCCCTCTCAG
16551 CCATCAGGAA CCCACCCAGG TTCTCTGAGG AGGGTCCAGT TTGGCTCCTG
16601 GTTCATGATC TGCTGCCCTT GTCCCTCATT CACCAGCCAC CCTAGGACAG
16651 GAGAAGAAAT AATACCAGTG CCCCACACCA TCAGGCCAAA CAGAGAGCCC
16701 ACGGGACACC TTGAATGAAT GTATCCATCT GATAACTTTC CAGCAGCCAC
16751 CGCCAATGGC GGGAGTCAGC AAACCTCAGA GCTGGCTCAG ATAGAGGCAA
16801 GCCAGGGGAA CAATGGGCAC AGAGAGTGTT CGGACTGCCT TCACCATCAA
16851 CCAGGCGCAG GGCAGGCCCC ATACCCAGCC TTGGGCCTCA GCCGGCTTCC
16901 TTAGCCAGGA TCTGGAGTCC AGGCCAGCCT TGGCTGAAGC TCTAGACTCC
16951 CTGAGCCTCC ATCCTCCCCT GCAGCTTCTG TCTGAAGCCA CAAAGAAGTC
17001 TGAGAATCTA AGCTACTGAA AGAAAAGATC AGCCGGGCGT GGTGGCTCAC
17051 TCCTGTAATC CCAGCACTTT GGGAGGCCAA GGCAGGTGGA TCACAAGGTC
17101 AGGAGTTCAA GACCAGCCTG GCCAACATGG TGAAACCCCG CCTCTACTAA
17151 AAATACAAAA ATTAGCCAGG TGTGGTGACG GGCCCCTGTA GTCCCAGCTA
17201 CTCGGTAGGC TGAGGCAGAG AATTGCTTGA ACCCAGGAGG CGGAGGTTGC
17251 AGTGAGCCAA GATCGCGCCA CTGCACTCCA GCCTGGGCAA CAGAGTGAAA
17301 CTCCATCTCA AAAGAAAAAA AAAGAAAATA TCTAGCCCCA CAAGAAGGGG
17351 CCATGGTGAC TTTAAGTGCC CGCCACGTTG GCAAAAGTCC ATTTCCGCTC
17401 CACTTCCCAG AGAAACCGTC AGCCAACACT CCAGGGAGAA GTGGTGTGCT
17451 TTGCTGCTAT TTTTGTCTTT GGCTGCTGGG CTCTCAGGGT TGCTTATTTG
17501 TTTGGCTTCC CCTCTGAAGT ACGTTTTGTG AATCACTTTT GAGACCCACT
17551 CAGAACATTC CTTTCCTTTT GCCTCCCTAC CCCAACAACA CTTCTAGCTG
17601 AGCTCCACCT ATGGGAAGAT CGGCGTGAAG GTCTTCTTGG TGAACATCCA
17651 TGGTAAGAGA AAGAGGACAT TTAGGGACTG AAAGACTGGC AAGGAGTGTG
17701 GGGTAGGAAC AGGTTGGTGG GGTCTGAATA GTGAGGAGGT TGGAAACGAG
17751 AGCACCCAGC TATCCCCCAC AAGCTGCTGC CTGCTCATAA AAGCTTCAGG
17801 TACAAGTCCA AAGAGACTGG TCAGATTGCA TAAACATCCT AGGGGCCTTA
17851 GTGACAGAGT GGGGGTGAGG AGGTCATGGA GTTACAGAAG GACAGCTAGG
17901 ATTCTAATCT ACCCCATAAC TAATTTGCCA CGTATCCTTG GCCGAGTCAC
17951 TTTATCTCTC AAGGGATCTA TTTCTACCTA TGTAAAACGA GAGGGTTGAC
18001 TAGATGGATT TGGGGATCCT CTCCCAATCA GAAACTCTGT GAATCGATAT
18051 AGGCATAGAG CACACGGTAC CCTAATTCCC CAGGGAACAT ATAAATATGC
18101 AGTTTTGTAG GCATACAGCC TCCAAAGGGT GCATATACAC AGCCTCAAGG
18151 ACGTGGCCAC AGGGCAGCAG ACATTTACAT GACTAGCATG TACGCAAAGT
18201 GCAGAGATGT GGGAGCAAGT GCACACAGAC ACACAGGAGA ATGTGAAGGG
18251 GCACATACAC ACACACCCAG CTCCCTGCAC TGGGTCAGAC CCCCTCCAGC
18301 AGGGCTGCAG TTCCCAAGCT CCGCATGGCC ACGTTCGGGG AGAGAATCTG
18351 CAGTGGCAAT GACCTGCTAT GATATGTTCT GGAGTTAGAA GCAGTGGATT
18401 CTCCCCAACC TCACTGGACA CCCCCTTAGG AAACCATCTC TAGGATTAAG
18451 AGTAATCCAC ACAAACTTCC AATGCCACAC ATTGGAAGTT GCTGGAAAGG
 18501 TCTGGGAAAA CAAGAGGAAG GATGGGTCCT TGGGGGATAG AACTGGCAGC
 18551 GGCCTCTTCA AGGATGGCTT AGGCTTTTCC ACTCGAATCA CCACAAAGTA
 18601 CTGACTCCCT AAATCAAACT GCTTCCTTCT GCTCTGGGTT GAAACTTCAG
 18651 CATCCTCAAG TTCATGTTGC CCTCTGCCGT CCAGAACTGA TATTGCACTG
 18701 CCAATGCCAT GGCCCTCAGA TACAGCAAGA GCTGGGACCT CAGGCCTCTC
 18751 CCATCCCTGC TCTGGTCTCA CTATCTTCCC CACCCCCAGC TCCAATCCAC
 18801 AATGGCTGTT ATCTTTCTGA AGGTGATCTT TTCTCCTTCT AGCCCAGGTG
 18851 TACAATGACA TTAGCCATGG AGGCGTCTTT GAGGATGGGA GTCTAGAATG
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18901	CAAGCACGTC	TTTCCCAGCA	TACATGACGC	AGTCCTCTTT	GCCCAGGCAA
	ATGCTAGAGA				AAGGTTCTTG
	CACCTGGGGA			GAAATAGCAG	GACCAAGAGG
	CATTATTAGA		GAGAAGGTTT	AAGTTCCAAT	ATCAAGTCTG
		TTTCTGAATC	TGTTTCCTTA	TCTATAGAAT	GAGCACCATC
	O OLUM	ACCTACCTCT	CTGCATTTTT		GTTTTAGGGT
		TTACATCTTT	TGTGTCACTT		TGTGTATTGT
19201		TATCAATATA			ACCCAAAGCA
			GCTGGCATCG	TTCCCTGCCT	CCTCCTCATC
19301	TAGTAGAGCA			GGGAGGGGAG	TAAGCCTACC
		GGGGGCTTTC	GGGAAGGGAG		GGGATAAAGA
19401	CATTTTAACT	TACCGGAGCT	TAGAGATTTC	GACATTTAAT	TTACTAGCTC
19451	GATTGGGTCT	GAGTTTTGTC	TCAGCTTTTT		ACTCCAGAAG
19501			TACAAATAAC		
19551	ACTGGGGAGT	CAGAAAAATC	CTACCTCCTT	GGGGTCCCTG	
19601	CAGTCATCTC	TAGCCCTCAG		CAGCTCAGCT	CCTGCCCTTG
19651	GCCTCCCAAG		TGCCCCAGCC	CTGGGTAAAA	
19701	CCCTCTGTGG	GTCATAAGAA	AGGCTTTTCT	GGCCCTAGAG	CAATGATTTG
19751			ATGAAGGTGA		TCTAAGTGCT
19801	GAAAGACTGC	CCAGGAACAC		GGCTCCTGCC	CTCCATGCCT
19851	AGAGGGAAAC		CAACGGGCTT	TCCTGCTTCG	TGAAATTTGT
19901			TTCTGGAGGA		
19951		GTTCAGCTAC		ATGTATACTT	GATTAGTCAT
20001	AGCACTTATA		ATTTTATATA		ACATATTATA
20051	GACCATTCAC		CACACACATA		TTTTCAACAG
20101	CATTGTGAGG	GACAAAGCAG	GCAAAGTGAG	• • • • • • • • • • • • • • • • • • • •	AGACTTTAAC
20151	AGATTAGAAA	ATATATTCCC	AGGAGGACAG		AGGTCAGGCA
20201	GCTAGCCAAT	AGTTTTTCTA	AGCTGAGTAA	AACCTTCCCT	GCCTCTAACG
20251	GCCCACAAAG	GAGGGAAGAC	CGCGATACAC	ACCTGTCTGG	TATAAGGGGG
20301	AAGACCACAG	CCGTGCTGTT	TTTGTGAGGC	AGGTAAGGGA	AGGGGCAAGA
20351	GGATAAGTCA	TGTGTCAGGA	AGCAGCGTCC	AACCAGAGCC	GGCCACCTGT
20401	CCCTTTTCCT		ACCAACTTTG	CTGTTCAGTC	ACTGAAGCTC
20451	ATTCTGCACT	GGCTTCCTCC	CTTCCAGGCT	CCAGGGGATG	CTGAGCTCTC
20501	CTTGTACGAC	TCAGAGGAGG		CTACTGGGAC	TTAGAGCAGG
20551	TGAGCTGAGG	GAAGGGGCTG	TGAGGGTGGG	AGCAGGGCGA	AGAGGGGAAG
20601	GATGGGGTCG		CAAGGCGTTC	ACTCAGCTGT	CTCACCTCCA
20651	GCCCAGAGCA		AGGCCACAAA		CATCTTTGTT
20701	TTTTTTCTTT	TCCTTTTCTT		TTTTAATTTG	AGACAAAGTC
20751	TCACTCTATC	ACCCAGACTG		GCATGATCTC	AGCTCACTGC
20801	AACCTCTGCC			CCTGCCTCAG	
20851	AGCTGGGACT	TCAGGCCTGC		TTTTTGTATT	TTTAGTAGAG
20901	ACAGCTTTTC	ACCATGTTGG			CGATCTCAAG
20951	CAATCTGCCT	GCCTCGGTCT			GCATAAGCCA
21001		CCTTTGTTTT		ACTCCCTGAA	
21051	CCCACACCCT	GAGTCACTGG	ACCAAGTCCT	AGAGAACCAG	TATCTATTCT
21101	ሚለጥጥርጥርር Δ Δ	CACATCACCC	ACGTGACCCT	GAGCAAGCCA	CATACACCCT
21101	CCCCCTACT	TTTTATCATC	TGTGAAATTA	GGGGAAACAT	AGGTAATACC
21201	TGTCCCATCC	ACCACACAAC	ATTGGCAGGG	CAGTCACTTG	TTCTTTCATT
21201	አለምምሮልርሮልር	GTATTTATGC	CGTACCTACT	GTTTGCCTGA	CACAGTTCAG
21201	CATCCCCACA	TACCACTGAC	CAAAACAAAG	GCCTCTGCCT	TTTAGAAACT
21301	TACCTTATCC	TAGAATAGAT	GGATTTNNNN	NNNNNNNNN	NNNNNNNNN
21.401	MINIMINIMINIMINIMI	MINIMINIMINININININININININININININININ	NNNNNGTCT	ACAAATGAAT	TATTATTGCA
21401	TOTOCACAAA	CCTTAAGAAC	TAAAAAATAT	GTGGCTGGGT	GCAATGGTTC
21431	ACACCECEA	TCCCAGCACT	TTGGGAGGCT	GAGGTGGGCG	GACCACCTGA
21301	ACACCIGIA	TOCCAGCACI	CCTGGCCAAC	· ATCCCCAAAC	CCCGTCTCTA
21331	. GGTCAGGAG1	IIGAGACCAC	CAGGCGTAGT	CGTGCATGCC	TGTAGTCCCA
21001	CIAAAAGCAC	YCHCHCYCC YCHCHCYCL	CAGGCGIAGI CATGAGAATCA	CTTGAACCTC	GGAGGCAGAT
Z1651	GUTACTUGGA	AGICIGAGG	TGCCACTGC	. CTCCACCTTC	GGTGACAGAG
ZT/01	GTTGCAGTGA	A GCCGAGATCC	A ACAAACAAA	CICCAGCIIC	AAGATATGTG
21/5]	CAMAMOACACA	, ICHAMAMCAE	CCATAGGGC	· CCTCCATTA	CACCACCCC
ZT80]	L GATATGAGG	AICHCCAIC	AAACCAGAT	Z ACTACCATIA	CACAAATCTC
2185]	L CCAATGCCCT	GAATTAAAA	AAACCAGATO AGTGTCTCT(2 WOIWGGIIIG	, TTCCCATTCT
21901	L GCTTTGGGTC	. TATGAGAAG	CHCCHCHCV	/ #CCC#C#C#C#(DCAGTGCTG
21951	TTTTGACATT	GAGUTUCATO	G GTGCTCTGA	7 TCCGTCTCTC	, ACACTGOIGE A CACAMTMCC
22001	L TGGCAGGTG(GACAGATTA	G AAAATAGAGO	. IGGAGCCACA	7 GUGUIIIGG

22051	AGACTGATTT	CGGTGCCCTC	TTGGAATCTC	CAGCACATTC	CAAAAAGCCT
22101		AAAATAGCTT	ATCAACGTGA	GAAAGGACTT	CAGAGCTTGT
22151	CTACTGCCAA	CCCTCATTTT	ACCCAATGAG	GAAAGTGAAG	CTATTAGGGG
22201	GCGAGGGACA		CACACAGCAC	ACAGGAGGTG	ATTCACATGT
22251		ACCTGCTCCT	GCCACGCTGG	ACTGGTTCAC	CTCCTAGGCT
22301	GACCCTGCCT	CTCCCCTGTT	CACACACACT	CTCGCACACA	CACACACACA
22351	CACACACACA	CACAGGTGCT	TTGTTCTGGC	CAGGGGTTCC	TAGGGTCACC
22401	TCTTGGTTGC	AGCCACTGTG	ACCCCAACTG	GTCTAACCTC	TCTCTTCCCC
22451	TCCCACTTCC	TTCCTGTGGT	TCCTGCAGGA	GATGTTCGGG	AGCATGTTTC
22501	ACGCAGAGAC	CCTGACCGCC	CTGTGAGGGC	TCAGCCAGTC	CTCATGCTGC
22551	CTACAGAGTG	CCTGGCACTT	GGGACTTCCA	TAAAGGATGA	GCCTGGGGTC
22601	ACAGGGGGTG	TCGGGCGGAG	GAAAGTGCAT	CCCCCAGAGC	TTGGGTTCCT
22651	CTCTCCTCTC	CCCCTCTCTC	CTCCCTTCCT	TCCCTCCCCG	CATCTCCAGA
22701	GAGAGCCTCT	CAGCAGCAGG	GGGGTGCTAC	CCTTACAGGA	GTGAGAGTCT
22751	GGTGAGCCCA	CTCTTCACCC	GTCAGGCCCT		GACAAGCCTC
22801	CTGCTCACTC	CACCCCACCC	ACCTCTGCCC		AGCTGAAGGA
22851	CACCTTGACT	TCCAGCTTTT	ACGAGTGAGC		AGGACAAGTA
22901	CAACTGTGCT	GGCCTGCTGT	ACAAGCTTCA	AAAAGTGTCC	CAGAGCCCAC
22951	ACGGCTCGGT	GTCAGATGGT	GTCAGGCTGT	CACGGACATA	GGGATAAACT
23001	TGGTTAGGAC	TCTGGCTTGC	CTTCCCCAGC	TGCCTCAACT	CTGTCTCTGG
23051	CAGCTCTGCA		ATGTGCTCTC	CACACCCAGG	AGTCTAGGCC
23101	TTGGTAACTA	TGCGCCCCCC	GTCCATCATC	CCCAAGGCTG	CCCAAACCAC
23151	CACTGCTGTC	AGCAAGCACA	TCAGACTCTA	GCCTGGACAG	TGGCCAGGAC
23201			CCTCCCCGGG	GACAGCCCAC	TAAGGTTCTG
23251	CCTCAGCCTC		ACTGCCCTCA	GAGGCTGCTC	CCTTCCCCTG
23231	GAGGCTGGCT	AGAAACCCCA		TGGGTAGCTG	GCAGAATCAT
23351	CTGGCATCCT		ACCAGTTATT	CTGCACAAAA	CTTTTGGGAA
23331	TTCCTCTTTG	CACCCAGAGA	CTCAGAGGGG	AAGAGGGTGC	TAGTACCAAC
23451		CGGATGGGAC	CTGGGCCCAG	ACAGTCCCCC	TTGACCCCAG
23501	GGCCCATCAG	GGAAATGCCT	CCCTTTGGTA	AATCTGCCTT	ATCCTTCTTT
23551		GAGCCAATCA	TGTTAACTCT	TCCTTATCAG	CCTGTGGCCC
23601	AGAGACACAA		CTGTAGGCAA	AGGTGGAAGT	CCTCCAGGGA
23651	TCCGCTACAT	CCCCTAACTG	CATGCAGATG	TGGAAAGGGG	CTGATCCAGA
		CTGCACAGGA	*	ACACCCTTAG	GACCTCAGGC
23701	TTGGGTCTTC CATCTTCTCC			TTAAGTTTTC	CATATGTACA
23751		GAGAGGAACC	CTACTGTTGA	CTTGAAAATA	
23801	AGGAGGTATT ATGTGTAAGT	•	ATTTCAGTGG	AAATGCACAG	
23851	GGCCTCTCAT	CACTGCTTTT	CTCAAGCTTC		CAACCCCTTC
23901	CCTAACAGGT	TGGGCTGGCC			
23951	TCAGCCAGAC	CTGCGTTGTG		TTGAGTGAGC	TGGTCAGCTA
24001			AGGAGGGGGT	GCTGGCCAAG	
24051	ACAAGTCTTC			AATTCATTAT	GCCATCTGGC
24101	TTCTTGGCCC		=	AGGACAATGT	TATCTGGGAT
24151			AGTGCCAAAT	TCCAGGAGGA	
24201				ACCTCCTTCC	
24251					
24301				CCCTGAGGAC	
24351				CCAGACCAGC	
24401					GGAGAGATCT
24451	GCCACATGTC			101100010110	50.10.10.11.01
24501	GOCACAIGIC	, lubuuulluu	. HOROCO		

FEATURES:

Start: 1997
Exon: 1997-2121
Intron: 2122-4732
Exon: 4733-4872
Intron: 4873-5004
Exon: 5005-5115
Intron: 5116-5781
Exon: 5782-5957
Intron: 5958-7770
Exon: 7771-7935
Intron: 7936-8470

8471-8623 Exon: Intron: 8624-8917 Exon: 8918-9000 Intron: 9001-9777 9778-9925 Intron: 9926-10221 10222-10335 Exon: Intron: 10336-10539 10540-10617 Exon: Intron: 10618-11197 Exon: 11198-11293 Intron: 11294-13338 Exon: 13339-13445 Intron: 13446-14214 Exon: 14215-14284 Intron: 14285-14400 Exon: 14401-14493 Intron: 14494-15980 Exon: 15981-16262 Intron: 16263-17597 Exon: 17598-17652 Intron: 17653-18842 18843-18988 Exon: Intron: 18989-20477 Exon: 20478-20549 Intron: 20550-22478 Exon: 22479-22523 Stop: 22524

CHROMOSOME MAP POSITION:

Chromosome 1

ALLELIC VARIANTS (SNPs):

	117/117/11	(0111 0) .					
DNA					Protein		
Position	Major	Minor	Domain		Position	Major	Minor
48	С	G	Beyond (ORF(5')			
132	G	A	Beyond (
724	A	C	Beyond (
1558	С	G	Beyond (
1577	A	G	Beyond (ORF(5')			
2487	С	A	Intron				
2634	T	C	Intron				
4352	A	G	Intron				
5157	A	С	Intron				
5658	A	${f T}$	Intron				
5945	T	С	Exon		180	T	T
6281	С	T	Intron				
6452	G	C	Intron				
6610	T	G	Intron				
7247	${f T}$	С	Intron				
7360	A	G	Intron				
7644	A	T	Intron				
8127	A	С	Intron				
8317	G	A	Intron				
9079	G	A	Intron				
9537	G	T	Intron				
12302	С	G	Intron				
12354	С	T	Intron				
12487	С	T	Intron				
13198	_	A	Intron				
13257	A	G	Intron				
14541	G	A	Intron				

14545	A	G	Intron				
15041	С	A	Intron				
15053	A	С	Intron				
15065	A	G	Intron				
15108	A	C	Intron				
16274	-	G	Intron				
17424	С	T	Intron				
17627	G	A	Exon	•	657	V	V
18427	${f T}$	С	Intron				
18813	С	G	Intron				
19035	T	С	Intron				
19182	${f T}$	С	Intron				
19508	-	GC	Intron				
19571	${f T}$	GC	Intron				
20147	T	G	Intron				
20180	G	A	Intron				
20584	A	${f T}$	Intron				
20717	${f T}$	С	Intron				
20894	A	G	Intron				
21787	_	A C	Intron				
22264	T	С	Intron				
22338		CA	Intron				
23363	T	С	Beyond OR				
23688	G	A	Beyond OR				
24210	A	С	Beyond OR	F(3 [†])			

Context:

DNA Position

48

CTGGGTTCCTATGTGGGGAGGTCATGCTCCCCACTCATTGAGCCCCC

[C,G]

[G, A]

TCACACTTTACATTTTACACAACCCCTTCTTATCCATTAACTCATTTGATCTTCACAACA
ACCCTGTGAGATATGTCTGTTACTCCCACTTTAGTGATACAGAATCTGAGGTTTGAAAAG
TAATGCTGACCATTCTGCCTCATTAATAAAAGCAGGATTAACCCAGGCTCCTGGACCCTT
CCACAAAAGGCATTAAGCAACCTGCTCCCCTCTGACAACCTCCCCTGTCACCCAGGCTCT
CCTCTGGGAAGTTGGGGGCATCTCTAGCCCCCAAGTAGTTACTCATTTTCAACCCCATCT

1558 TCAGCTCTGCCCATCTCAGCTCCTGGAACGTCAGCCAGGTTGCGCAAAAAGTGAGGAGGA GAGGAGCGGCAGTACACAAGGGTGGGGGAAAGATTAGGCACAGGAAGCCGTGGGAGAGAG AGCCGGCAGGTGGACCATCCTGGTTTCCCCACACACCATTGTCCCCCTGGGAAACCTG TTGGTGAAGTTCTAGATGTCTTATCCAAGAAGGGTCCTCTTGAGGTCATCTCAGCTATCCCCCTGCCTCTAGGCAAGCTGTTTTCTGTTTCTTCCAAGCTGACTGGCTGAATGGTAGGAG

2487 ACACGCTTCTGCACTGGTATCCCTAAGATGGGGTTAAGGGAAGCCCTGGGGAAGTGAGG
TTCTGAATGATGATTTAAGATCCTACAACCTCATCTGTACTGAGACCCCCAGGGAGGAT
GGGGAGCAGGAGCAAGAACCATCCAGAAGGGTTATATGGCATTCCCAAACCCCTGCATGG
CATCTCCCATATTCTCAATTCACCCGGGTCTCTCTGGGTTTGTTAAGGCATGGTAGATGA
GCATCTACGTTATGGAGGGGTGGGGAGCATCAGAGCCCTTACTCCATGCCCTGTTCCCTC

CAAGGATGGGAGGTGTGGCAAAGGGGCCTCGGGAGATTTTCCATCTGCATTTCTCCTGGAG TTGTTCCTGGTCAGTCCTAGGGGAATGGTCACTGTGAATGTCATTTCCAGGTCCTCGGTG ACCTTGGAGAAACCACTGAGCCTCTTTGAGTTCAGTTAGCATTACCTGTTCCATCTTCCT CCTAGGAATGAGAGAGACTTAGCAGAACAAGATATACCATATGCTATAACATGCTTAA ACAGATGTGAGAAATCACCATCTAACTCCCTGGTTGGTCCCAGCCGGCCACTACAGGGAC

> GCCATCATCCAGGTGAGGGGGCAGCCCCCAACCCTGCTAGAAGGGCATCAGACCACCCTG CCCCTCCCTCAAAGCCTTAGCTTTGATGCTAAATCTGATTTAGGGGGCTGGGTGTGGAGG CTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGAGGAGGGTGGATCACTTGAGGTCAGG AGTTTGAGACCACCTTGACCAACGTGATGAAACCCCATCTCTACCAAAAATACAAAAATA ATCCAGGCTTGGTAGTATGCGCCTGTAGTCCCACCTACTCAGGAGGCTGAGGCAGGAGAA

GCTAGAAGGGCATCAGACCACCTGCCCCTCCAAAGCCTTAGCTTTGATGCTAAATC
TGATTTAGGGGGCTGGGTGTGGAGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCTGA
GGAGGGTGGATCACTTGAGGTCAGGAGTTTGAGACCACCTTGACCAACGTGATGAAACCC
CATCTCTACCAAAAATACAAAAATAATCCAGGCTTGGTAGTATGCGCCTGTAGTCCCACC
TACTCAGGAGGCTGAGGCAGGAGAATCACTTGAATCCGGGAGGCAGAGGTTGCAGTGAGC
[C,T]

GACCATACAAAAAAACAGCTGTACCTGGTTAAACTGTCCTGAGCTTTAAACCTGTAA
AAGACTCACAGCCTCTCCCATTATCCCGTGGAGAAACCCAACTCTCTGCCAGCATAGTC
TTGCAGACTGCTAATTTTCTCTAACATCCCTCACTCCGCTCCAGCCTCCTCTGCTCCAAG
CCACAGCAGCAGTTGCACAACATAAATTGAGCTTCTGCAAATGGTTGCAAAGGATTCTGC
TAGGTTTTATGAAGGGAAGCACAACATGACAGAATGCAAGAGCAAAACACAGTCCCAGAG

7247 GACACAGAGCAGAGTCACGGAGGACCTCAAAGAGGAGGTGACACTCCACCTCTCTTAAAG
GATGAGAACTTAACCAGGAACAAGGTATACAGAGGATGGTCCAGGCAGAAGGGAACAGTG
CCTAAAAACACTGAGGCCTGAGAGAGTGTGATCTGCGCAGGCAAAGTAAGGGGCTTGGTG
TGGCTGGAGGGTAGAGGGCCCAGAAGAGGATGGAAAAGTAGGCAGGAGCCAGACAATGAG
ATCTGGGGTCTGTTCTCTGACAGCGACTTTGGGTCTGATTGGCAGTTTATAAGGATCGTT
[T.C]

GGGCTACACAATGATGAGTGGGAGGTGGATTAGAATCAAGGCAGGGGACCTGTTGGGAGA CTCTGCAGAGGCCCAGGCAGGAATAATGCAGGCGAAGACCAGGTAGAGAAAGAGATGGGG CTGGACTTGAAAAGAATGTTTTACCAGGAGCTTGGTGATAGACTGGATGTGGGAGGTAAG GGAGGATGACTCTCAAGTTTTTGGTTGGGCAACCAGGTTAATGATGGTGTCATTTACTGA GAGAGAAAACACTGGGGGAGGACTAGACTTATTTTACAGATAAGCCAAAGCCAGAGAGGT

7360 AACAGTGCCTAAAAACACTGAGGCCTGAGAGAGTGTGATCTGCGCAGGCAAAGTAAGGGG
CTTGGTGTGGCTGGAGGGTAGAGGGCCCAGAAGAGGATGGAAAAGTAGGCAGAGCCAGA
CAATGAGATCTGGGGTCTGTTCTCTGACAGCGACTTTGGGTCTGATTGGCAGTTTATAAG
GATCGTTTGGGCTACACAATGATGAGTGGGAGGTGGATTAGAATCAAGGCAGGGGACCTG
TTGGGAGACTCTGCAGAGGCCCAGGCAGGAATAATGCAGGCGAAGACCAGGTAGAGAAAG
[A.G]

GATGGGGCTGGACTTGAAAAGAATGTTTTACCAGGAGCTTGGTGATAGACTGGATGTGGG AGGTAAGGGAGGATGACTCTCAAGTTTTTGGTTGGGCAACCAGGTTAATGATGGTGTCAT TTACTGAGAGAAAACACTGGGGGAGGACTAGACTTATTTTACAGATAAGCCAAAGCCA GAGAGGTGATGTGACAGAAAGGCCCATGCTCTAAAGGAGCTGAAGGTCTGATGGCAGCCA TGTAGAGCACAGTGAAGGCAGGTGAAGGTCACAGATGGTCCAATTCCCTCAAGCTACTG

CATCCGGGGCTTCATGACGGCCGCCCGGCCTGCAGATCCTGATTTCGGTGCTCAAGTACAT CTTCGGACTGACCATCCCCTCCTACACAGGCCCAGGGTCCATCGTCTTTGTGAGTCTGGG GATGCACCCCTGCCATTGGAGCAAGGCTCCAGCAGACACATGAGGAGGATGTACTGTTTT AAGATGTCGTGAGCTCCTCATTGCAAGGGCTGGCTTAGCTGTTGTTCAGAGAGGATTCTG AGGGGGTTTCTGTCTTTGGGAGGGTCAAAGTCATGACTCACAGAGGGTTCTTGGTAGTTAAT

> > FIGURE 3, page 13 of 20

9079 TTCTACTGCTCTAATAATTCCCCCTAAGGAGGCAGGGGAGTGGGATTCAGGGTCCCCAGA
GAAAAGGGAGACTTGAGAGAGACGCCTGCCCTGGCCCACCTTAGGGCCAATCCCCATTC
TCCACTCTGGGGTTTGCAGGTGGTGGTGGCAACAGCTATCTCCGGGGGCTGTAAGATGCC
CAAAAAGTATCACATGCAGATCGTGGGAGAAATCCAACGCGGGTGAGTCCAGGTGGCCCA
GAAGCCTGGCCCACCCGCACCTCATGCCCCACTAAGGCCTGAGCTCGGAGAGGGAGACAA
[G_A]

ATGAACTCTATGAAAGTGCAGTCGAAACTGTATGACACTGACCATGTATGAATTATTACT
ATTACCGTTTCCTGAGAAGGGCCGCACAACCAGCCAATGTAGGCTATTTTATGAGAAATG
AGTCTTAACTGCCACACTCCCCTTATAAATCTCATTCAACTGATGCTGTTAAACAAAGCC
TCTCTGAACAGCCGCTTGCTGGCTCTTTGCCTTGCTCTAATGCATTGGTTCTTTTGTCCAT
GTAGAAAGGGAACTATTAGGTTCAACCAGATTCATGAAGCATCCACTCTGTGCCAGGCAC

9537 AACTGATGCTGTTAAACAAAGCCTCTCTGAACAGCCGCTTGCTGGCTCTTTGCCTTGCTC
TAATGCATTGGTTCTTTGTCCATGTAGAAAGGGAACTATTAGGTTCAACCAGATTCATGA
AGCATCCACTCTGTGCCAGGCACCATGCTGGGCCCTGGGAGAGAGGGGTGACGCTTGTC
CTGCAGGGTTGGAACAGGCAAGGGAGGGAAGACCACATAGCACCAAAGGTCTAGGGGTCT
GTGGACTCGTGAGCATACAGGGTTCAGAATCTGGGAGTTAACAAACGAGGCCCTACCACA
[G, T]

12354 GAAACCAAGGCTCAGAATGGTTAAGTAAATTGTCAAAGGCCACAGAGGTAGGGAGTGGTA
GAGTCTGGATTAAAACTCCAAGTCCTGGACTCCAGACCTCTAGGCTGTACTGTCTCATAG
GGAAGGCAGTCTCACCCACCTAGGGCAGAAAAATCCTTAAAGCCAGAGAAGTGAGT
GGCTCATCTGTGGTCACCCAGAGAGACAGTGATGAGGACAGGGAGAAAAATTATACCTCA
GTTCCCAGCCCAAGGATCTGCTTTGACCATAACCCAACAAGCCCCCGCTATGGTGGTATT

 ${\tt TAGATGCCACCTCCCTGTGTGCTGGGGCTTCTACTAAAAACACAGACAAGATCAGGCAACCACAGTCAATCTAAGGGAAAGAGGGAAAGTGTAACCAAAGCACAAATACATAAAATATTGC {\tt -, A}$

AAAATGCTATTTAAAGAAAAAAAGAGAAGAGAGGCTCTGAGGTTGTACTAACAGAGAAT GGCCTTGGCTAATCCAGGAAGACTTCCTGAAAGAGGTTGTTTTTTCCCCAGGTCTGCTTT TGACATCTCTCTTTTCACAGTGCATCTGGGTAGTGAGCTTCCTCCTCCTTCTTCCTCA GCCTGCCCTATGGTGTGGCAGTGGGTGTCGCCTTCTCCGTCCTGGTCGTGGTCTTCCAGA CTCAGTTGTAAGTGATAGCTTCCGCCCTCCTAGGCCCACAGTCGGTTCCCTGGGCCAGCC

TGGCCTTGGCTAATCCAGGAAGACTTCCTGAAAGAGGTTGTTTTTTCCCCAGGTCTGCTT
TTGACATCTCTCTTTCACAGTGCATCTGGGTAGTGAGCTTCCTCCTCCTCCTTCTTCCTC
AGCCTGCCCTATGGTGTGGCAGTGGGTGTCGCCTTCTCCGTCCTGGTCGTGGTCTTCCAG
ACTCAGTTGTAAGTGATAGCTTCCGCCCTCCTAGGCCCACAGTCGGTTCCCTGGGCCAGC
CCGCAAAGGGCTTCCATGCCACGGCCTGGCTTAGTCCACTGTACCTTCCACCTCTGGGCC

> GAAAATGGAAGCAGAAGGGCGGTGGGAGCTGAGAATAGGCCACTCCCATAGAGGGTGGAG GTCAAGATTGCTGTTGGCTCTCCCTGCAGACAGGCATGGACCCCCAGAAAGTATTACT AGCCAAGCAAAAATACCTCAAGAAGCAGGAGAAGCGGAGAATGAGGCCCACACAACAGAG GAGGTCTCTATTCATGAAAACCAAGGTGAATGAAGGCCAGAAGCAGCCCCGTGCCCTGCT CTCCTGCCCATTCTGATACTGCCCCCTGTTACTCATGGTACCCTGGGGGCCCCGCTTCCC

ATGGAAGCAGAAGGCCGTTGGGAGCTGAGAATAGGCCACTCCCATAGAGGGTGGAGGTCA
AGATTGCTGTTGGCTCTCCCTGCAGACAGGCATGGACCCCCAGAAAGTATTACTAGCC
AAGCAAAAATACCTCAAGAAGCAGGAGAAGCGGAGAATGAGGCCCACACAACAACAGAGGAGG
TCTCTATTCATGAAAACCAAGGTGAATGAAGGCCAGAAGCAGCCCCGTGCCCTGCTCTCC
TGCCCATTCTGATACTGCCCCCTGTTACTCATGGTACCCTGGGGGCCCCGCTTCCCACCC

> CCCAGCTAATTTTTGTATTTTTAGTAGATATTTGGGTTTCACCATGTTGGCCAGGCTGGTG TCAAACTCCTGACCTCAGGTGATCCACCTACCTTAGCCTTCCAAAGTGCTGGGATTACAA GCCTGAGCCACTGCGCCCAGCCTGGGCATTTTTCTTCTTGGATGAGGTGCTACCATCTCC CAGGGAAGCCACTGAACCCCCAAGGCCCTTCTCCATTTTCTGGCTAAGATAGGACATGGC CCATGGACTTTTGAACAACCCAGAGGGGGAACAGCAGTGAATTTCCTGGGGAACCCAGGC

16274 CTTCCAGACTGTCTCCCTGCAGGAGCTGCAGCAGGACTTTGAGAATGCGCCCCCCACCGA
CCCCAACAACAACCAGACCCCGGCTAACGGCACCAGCGTGTCCTATATCACCTTCAGCCC
TGACAGCTCCTCACCTGCCCAGAGTGAGCCACCAGCCTCCGCTGAGGCCCCCGGCGAGCC
CAGTGACATGCTGGCCAGCGTCCCACCCTTCGTCACCCTCATCCTGGACAT
GAGTGGAGTCAGCTTCGTGGACTTGATGGGCATCAAGGCCCTGGCCAAGGTGAGGCCCTC

AACACTCCAGGGAGAAGTGGTGTGCTTTGCTGCTATTTTTGTCTTTTGGCTGCTCTCCAGGGTTCTCAGGGTTGCTTATTTTGTTTTTGTTTTTGCTTCCCTCTGAAGTACGTTTTTGTGAATCACTTTTTGAGACCCCACCACAACAACACTTCTAGCTGAGCTCCCCTACCCCAACAACACTTCTAGCTGAGCTCCCCTATGGGAAGATCGGCGTGAAGGTCTTCTTGGTGAACATCCATGGTAAGAGAAAGAGACATTTAGGGACTGAAAGACTGGCAAGGAGTGTGGGGTTAGGAACAGGTTTGGTGGGGTC

> AAGGTCTTCTTGGTGAACATCCATGGTAAGAGAAGAGGACATTTAGGGACTGAAAGACT GGCAAGGAGTGTGGGGTAGGAACAGGTTGGTGGGGTCTGAATAGTGAGGAGGTTGGAAAC GAGAGCACCCAGCTATCCCCCACAAGCTGCTGCTGCTCATAAAAGCTTCAGGTACAAGT

AGGAAACCATCTCTAGGATTAAGAGTAATCCACACAAACTTCCAATGCCACACATTGGAA
GTTGCTGGAAAGGTCTGGGAAAACAAGAGGAAGGATGGGTCCTTGGGGGATAGAACTGGC
AGCGGCCTCTTCAAGGATGGCTTAGGCTTTTCCACTCGAATCACCACAAAGTACTGACTC
CCTAAATCAAACTGCTTCCTCTGTCTCTGGGTTGAAACTTCAGCATCCTCAAGTTCATGT
TGCCCTCTGCCGTCCAGAACTGATATTGCACTGCCATGCCCATGGCCCTCAGATACAGCA

> TTTCTGAAGGTGATCTTTCTCCTTCTAGCCCAGGTGTACAATGACATTAGCCATGGAGG CGTCTTTGAGGATGGGAGTCTAGAATGCAAGCACGTCTTTCCCAGCATACATGACGCAGT CCTCTTTGCCCCAGGCAAATGCTAGAGACGTGACCCCAGGACACAACTTCCAAGGGGTAAG GTTCTTGCACCTGGGGAATCCTAGGCTCCAAGGCACTGAAATAGCAGGACCAAGAGGCAT TATTAGAAAGAACACAGGAGAAGGTTTAAGTTCCAATATCAAGTCTGCCATTTCAGTTTT

19035 GGACCTCAGGCCTCTCCCATCCCTGCTCTGGTCTCACTATCTTCCCCACCCCCAGCTCCA
ATCCACAATGGCTGTTATCTTTCTGAAGGTGATCTTTTCTCCTTCTAGCCCAGGTGTACA
ATGACATTAGCCATGGAGGCGTCTTTGAGGATGGGAGTCTAGAATGCAAGCACGTCTTTC
CCAGCATACATGACGCAGTCCTCTTTGCCCAGGCAAATGCTAGAGACGTGACCCCAGGAC
ACAACTTCCAAGGGGTAAGGTTCTTGCACCTGGGGAATCCTAGGCTCCAAGGCACTGAAA
[T,C]

AGCAGGACCAAGAGGCATTATTAGAAAGAACACAGGAGAAGGTTTAAGTTCCAATATCAA
GTCTGCCATTTCAGTTTTCTGAATCTGTTTCCTTATCTATAGAATGAGCACCATCAACTA
ACATTACCTACCTCTCTGCATTTTTCTTTTATTTTGTTTTAGGGTTAAATGATAATTACA
TCTTTTGTGTCACCTTGAAAGCACTTTGTGTATTGTAAAAATTCTTTATCAATATAAGTTT
TCTGGTTGCACAAACACCCAAAGCATAGTAGAGCAGGCCCACTCTGCTGGCATCGTTCCC

> > FIGURE 3, page 17 of 20

> GAATTCCCCAAGGTCAGGCAGCTAGCCAATAGTTTTTCTAAGCTGAGTAAAACCTTCCCT GCCTCTAACGGCCCACAAAGGAGGGAAGACCGCGATACACACCTGTCTGGTATAAGGGGG AAGACCACAGCCGTGCTGTTTTTGTGAGGCAGGTAAGGGAAGGGGCAAGAGGATAAGTCA TGTGTCAGGAAGCAGCGTCCAACCAGAGCCGGCCACCTGTCCCTTTTCCTGCCACCATGC ACCAACTTTGCTGTTCAGTCACTGAAGCTCATTCTGCACTGGCTTCCCCTTCCAGGCT

20584 TGTCTGGTATAAGGGGGAAGACCACAGCCGTGCTGTTTTTGTGAGGCAGGTAAGGGAAGG
GGCAAGAGGATAAGTCATGTGTCAGGAAGCAGCCGTCCAACCAGAGCCGGCCACCTGTCCC
TTTTCCTGCCACCATGCACCAACTTTGCTGTTCAGTCACTGAAGCTCATTCTGCACTGGC
TTCCTCCCTTCCAGGCTCCAGGGGATGCTGAGCTCTCCTTGTACGACTCAGAGGAGGACA
TTCGCAGCTACTGGGACTTAGAGCAGGTGAGCTGAGGGAAGGGGCTGTGAGGGTGGGAGC
[A, T]

GTAGAGACAGCTTTTCACCATGTTGGCTGGGCTGGTCTCGAACTTCCGATCTCAAGCAAT CTGCCTGCCTCGGTCTCCTAAGTGCCTGGATTACAGGCATAAGCCACGATGCCTGGCCTT TGTTTTCATTCTTCTCACTCCCTGAAAGGCATCGTGGGGAGAGGGTGAGTCACTGGACCA AGTCCTAGAGAACCAGTATCTATTCTTATTCTCCAACACATCACCCACGTGACCCTGAGC AAGCCACATACACCCTGGGCCCTAGTTTTTATCATCTGTGAAATTAGGGGAAACATAGGT

TAAAAGATATGTGGATATGAGGGATCACCATCCCCATAGGGCCCCTGGATTAACACCACC CCACCAATGCCCTGAATTAAAAGAAACCAGATGACTAGGTTTGGAGAAATCTGGCTTTTGG GTCTATGAGAAGTAGTGTCTCTCTTTTTTGTGCCTCTTCCCATTCTTTTTTGACATTGAGCTCC ATGGTGCTCTGAATCCGTCTCTCACAGTGCTGATGGCAGGTGGGACAGATTAGAAAATAG AGCTGGAGCCACAGAGATTTGGCAGACTGATTCGGTGCCCTCTTGGAATCTCCAGCACA

22264 CTCCATGGTGCTCTGAATCCGTCTCTCACAGTGCTGATGGCAGGTGGGACAGATTAGAAA
ATAGAGCTGGAGCCACAGAGATTTGGCAGACTGATTTCGGTGCCCTCTTGGAATCTCCAG
CACATTCCAAAAAGCCTGGATAGGACCAAAATAGCTTATCAACGTGAGAAAGGACTTCAG
AGCTTGTCTACTGCCAACCCTCATTTTACCCAATGAGGAAAGTGAAGCTATTAGGGGGCG
AGGGACACGTGGAAGGTCACACAGCACACAGGAGGTGATTCACATGTAGATTTCAGCACC
[T,C]

GCTCCTGCCACGCTGGACTGGTTCACCTCCTAGGCTGACCCTGCCTCTCCCCTGTTCACA
CACACTCTCGCACACACACACACACACACACACACACAGGTGCTTTGTTCTGGCCAGG
GGTTCCTAGGGTCACCTCTTGGTTGCAGCCACTGTGACCCCAACTGGTCTAACCTCTCT
TTCCCCTCCCACTTCCTTCCTGTGGTTCCTGCAGGAGATGTTCGGGAGCATGTTTCACGC
AGAGACCCTGACCGCCCTGTGAGGGCTCAGCCAGTCCTCATGCTGCCTACAGAGTGCCTG

[-,C,A]
CACACACACACACACACACACACAGGTGCTTTGTTCTGGCCAGGGGTTCCTAGGGTCA
CCTCTTGGTTGCAGCCACTGTGACCCCAACTGGTCTAACCTCTCTTCTCCCCCACTT
CCTTCCTGTGGTTCCTGCAGGAGATGTTCGGGAGCATGTTTCACGCAGAGACCCTGACCG
CCCTGTGAGGGCTCAGCCAGTCCTCATGCTGCCTACAGAGTGCCTGGCACTTGGGACTTC
CATAAAGGATGAGCCTGGGGTCACAGGGGGTGTCGGGCGGAGAAAGTGCATCCCCCAGA

AATAGATACCAGTTATTCTGCACAAAACTTTTGGGAATTCCTCTTTGCACCCAGAGACTC
AGAGGGGAAGAGGGTGCTAGTACCAACACAGGGAAAACGGATGGGACCTGGGCCCAGACA
GTCCCCTTGACCCCAGGGCCCATCAGGGAAATGCCTCCCTTTTGGTAAATCTGCCTTATC
CTTCTTTACCTGGCAAAGAGCCAATCATGTTAACTCTTCCTTATCAGCCTGTGGCCCAGA
GACACAATGGGGTCCTTCTGTAGGCAAAGGTGGAAGTCCTCCAGGGATCCGCTACATCCC

23688 AAACTTTTGGGAATTCCTCTTTGCACCCAGAGACTCAGAGGGGAAGAGGGTGCTAGTACC
AACACAGGGAAAACGGATGGGACCTGGGCCCAGACAGTCCCCCTTGACCCCAGGGCCCAT
CAGGGAAATGCCTCCCTTTGGTAAATCTGCCTTATCCTTCTTTACCTGGCAAAGAGCCAA
TCATGTTAACTCTTCCTTATCAGCCTGTGGCCCAGAGACACAATGGGGTCCTTCTGTAGG
CAAAGGTGGAAGTCCTCCAGGGATCCGCTACATCCCCTAACTGCAGATGTGGAAAG
[G,A]

FIGURE 3, page 19 of 20

GGCTGATCCAGATTGGGTCTTCCTGCACAGGAAGACTCTTTAACACCCTTAGGACCTCAG GCCATCTTCTCCTATGAAGATGAAAATAGGGGTTAAGTTTTCCATATGTACAAGGAGGTA TTGAGAGGAACCCTACTGTTGACTTGAAAATAAATAGGTTCCATGTGTAAGTGTTTTGTA AAATTTCAGTGGAAATGCACAGAAAATCTTCTGGCCTCTCATCACTGCTTTTCTCAAGCT TCTTCAGCTTAACAACCCCTTCCCTAACAGGTTGGGCTGGCCCAGCCTAGGAAAACATCC

24210 TCACTGCTTTTCTCAAGCTTCTTCAGCTTAACAACCCCTTCCCTAACAGGTTGGGCTGGC
CCAGCCTAGGAAAACATCCCCATTTCTAACTTCAGCCAGACCTGCGTTGTGTGTCTGTGT
GTTGAGTGAGCTGGTCAGCTAACAAGTCTTCTTAGAGTTAAAGGAGGGGGTGCTGGCCAA
GAGCCAACACATTCTTGGCCCAGGAGCATTGCTTTTCTGTGAATTCATTATGCCATCTGG
CTGCCAATGGAACTCAAAACTTGGAAGGCGAAGGACAATGTTATCTGGGATTCACCGTGC
[A, C]